

FIGURE 1

CGGACGCGTGGGTGCGAGGCGAAGGTGACCGGGGACCGAGCATTAGATCTGCTCGGTAGA
 CCTGGTGCACCACCATGTGGCTGCAAGGCTGGTGTCTCCGGACACTACCTTCTAGG
 GTTTCCACCCAGCTTCACCAAGGCCTCCCTGTGTGAAGAATTCCATCAGAAGAATCA
 ATGGCTGTTAACACCTAGCAGGAATATGCCACAAAACAAGAATTGGGATCCGGCGTGGGA
 GAACTGGCCAAGAACTCAAAGAGGCAGCATGGAACCATCGATGGAAAAAATTAAATT
 GATCAGATGGGAAGATGGTTGGTGTGGAGGGCTGCTGTGGTCTGGAGCATTGTGCTA
 CTATGGCTTGGGACTGTCTAATGAGATTGGAGCTATTGAAAAGGCTGTAATTGGCCTCAGT
 ATGTCAAGGATAGAATTCAATTCCACCTATATGTACTTAGCAGGGAGTATTGGTTAACAGCT
 TTGTCGCCATAGCAATCAGCAGAACGCCCTGTCTCATGAACTTCATGATGAGAGGGCTTGG
 GGTGACAATTGGTGTGACCTTGCAGCCATGGTGGAGCTGGAATGCTGGTACGATCAATAC
 CATATGACCAGAGGCCAGGCCAAAGCATCTTGCTGGTGTACATCTGGTGTGATGGGT
 GCAGTGGTGGCTCCTCTGACAATATTAGGGGGCTCTCTCATCAGAGCTGCATGGTACAC
 AGCTGGCATTGTGGGAGGCCTCTCCACTGTGGCCATGTGTGCGCCAGTGAAAGTTCTGA
 ACATGGGTGACCCCTGGGAGTGGCCTGGGTCTCGTCTTGTGTGCCATTGGGATCTATG
 TTTCTCCACCTACCACCGTGGCTGGTGCCTTACTCAGTGGCAATGTACGGTGGATT
 AGTTCTTTCAGCATGTTCTCTGTATGATAACCCAGAAAGTAATCAAGCGTGCAGAAGTAT
 CACCAATGTATGGAGTCAAAATATGATCCCATTAACTCGATGCTGAGTATCACATGGAT
 ACATAAATATATTATGCGAGTTGCAACTATGCTGGCAACTGGAGGAACAGAAAGAATG
AAGTGACACTCAGCTCTGGCTCTGCTACATCAAATATCTGTTAATGGGGCAGATATGC
 ATTAAATAGTTGTACAAGCAGCTTCGTTGAAGTTAGAAGATAAGAAACATGTCTACATA
 TTTAAATGTTCCGGTAATGTGATGCCCTAGGTCTGCCCTTTCTGGAGAATAATGCAGT
 AATCCTCTCCAAATAAGCACACACATTTCATTCTCATGTTGAGTGATTAAATGTT
 TTGGTGAATGTGAAAACTAAAGTTGTGTCATGAGAATGTAAGTCTTTCTACTTAA
 TTTAGTAGGTTCACTGAGTAACTAAATTAGCAAACCTGTGTTGCATATTGGAGT
 GCAGAAATATTGTAATTATGTCATAAGTGATTGGAGCTTGGTAAAGGGACCAGAGAGAAG
 GAGTCACCTGCAGTCTTGTTTAAATACTTAGAACTTAGCAGTGTGTTATTGATTA
 GTGAGGAGCCAGTAAGAAACATCTGGTATTGGAAACAGTGGTCATTGTTACATTCA
 GCTGAACTTAAACAAACTGTTCATCCTGAAACAGGCACAGGTGATGCATTCTCCTGCTGTTG
 CTTCTCAGTGCTCTCTTCCAATATAGATGTGGTCATGTTGACTTGACAGAATGTTAAC
 ATACAGAGAATCCTTGATGGAATTATATATGTGTTACTTTGAATGTTACAAAGGAA
 ATAACTTAAACTATCTCAAGAGAAATATTCAAAGCATGAAATATGTTGCTTTCCAG
 AATAACAAACAGTATACTCATG

FIGURE 2

MLAARLVCLRTLPSRVFHPAFTKASPVVKNSITKNQWLLTPSREYATKTRIGIRRGRTGQEL
KEAALEPSMEKIFKIDQMGRWFVAGGAAVGLGALCYYGLGLSNEIGAIEKAVIWPQYVKDRI
HSTYMYLAGSIGLTALSIAIASRTPVLNFMMRGSWVTIGVTFAAMVGAGMLVRSIPIYDQSP
GPKHLAWLLHSGVMGAVVAPLTIILGGPLLIRAAWYTAGIVGGLSTVAMCAPSEKFLNMGAPL
GVGLGLVFVSSLGSMFLPPTTVAGATLYSVAMYGGLVLFSMFLYDTQKVIKRAEVSPMYGV
QKYDPINSMLSIYMDTLNIFMRVATMLATGGNRKK

FIGURE 3

GAAGGCTGCCTCGCTGGTCCGAATTGGTGGGCCACGTCCGCCGTCCTCGCCTCTGCAT
 CGCGGCTCGGGCGCTTCCACCTAGACACCTAACAGTCGCGAGGCCGCCGCGTCGTGAGGG
 GGTGGCAGGGGAGTCGGCGGTCTTGTGCATCTTGGTACCTGTGGGTGAAAG**ATGT**CGG
 ACATCGGAGACTGGTTCAAGGAGCATCCCGCGATCACGCGTATTGGTGCGCCACCGTC
 GCCGTGCCCTGGTCCGGCAAACCTCGGCCTCATCAGGCCGGCTACCTCTCCCTGGGCCGA
 AGCCTCCTTATCGCTTCAAGATTGGAGGCCAATCACTGCCACCTTATTCCCTGGGCCGA
 GTCCAGGAACTGGATTCTTATTGGTCAATTATATTCTTATATCAGTATTCTACCGA
 CTTGAAACAGGAGCTTGTGGAGGCCAGCAGACTATTATTCATGCTCCTTTAACTG
 GATTGATCGTATTACTGGCTAGCAATGGATATGCAAGTGCTGATGATTCTCTGATCA
 TGTCAGTACTTTATGTCGGGCCAGCTGAACAGAGACATGATTGATCATTGGTTGGA
 ACACGATTAAGGCCTGCTATTACCTGGTTATCCTTGGATTCAACTATATCATCGGAGG
 CTCGGTAATCAATGAGCTATTGAAATCTGGTGGACATCTTATTTCCTAATGTC
 GATAACCAATGGACTTGGGAGGAAGAAATTCTATCCACACCTCAGTTTGACCGCTGG
 CTGCCAGTAGGAGAGGAGTATCAGGATTGGTGTGCCCTGCTAGCATGAGGCCAGC
 TGCTGATCAGAATGGCGAGGCAGGACACAACGGGCTTCGACTTGAGGAC
 AG**TGA**AGGGCGGCCCTGGCAGCCGCTCTCAAGCCACATTCCCTCCAGTGCTGGGTG
 CACTTAACAACACTGCGTTCTGGCTAACACTGTTGGACCTGACCCACACTGAATGAGTC
 AGTACGAGACAAAGTTCTAAATCCCAGAAAAATATAAGTGTTCACAAAGTTTACGAT
 TCTCATTCAAGTCCTTACTGCTGTGAAGAACAAATACCAACTGTGCAAAACTGAC
 TACATTTTGGTGTCTCTTCTCCCTTCCGCTGAATAATGGGTTTAGCGGGTCT
 AATCTGCTGGCATTGAGCTGGGCTGGTACCAAAACCTTCCAAAAGGACCTATCTT
 TCTTGCAACATGCCCTCTCCACTTTCCAAACCCCCACATTGCAACTAGAAAAAGTTG
 CCCATAAAATTGCTCTGCCCTGACAGGTTGTTATTGACTTTGCCAAGGCTGGTC
 ACAACAATCATATTACGTTATTTCCTTGGTGGCAGAACTGTACCAATAGGGGAG
 AAGACAGCCACGGATGAAGCGTTCTCAGTTGGAATTGCTCGACTGACATCCGTTGTT
 AACCGTTGCCACTCTCAGATATTAAAGTACCAACTGAGTTCATGAGGCCA
 CAGATTGGTTATTAGAGATACGAGGGTGGTGTGGTGTGGTGTGGTGTGGTGT
 TCAAGACTGTAGTGGAGTTGCAGCTAACATGGTTAGGTTAAACCATGGGGATGCACCC
 TTTGCCTTCATATGTAGCCCTACTGGCTTGTGTAGCTGGAGTAGTTGGTTGCTTGT
 TAGGAGGATCCAGATCATGGTGGCTACAGGGAGATGCTCTTGGAGAGGTCTGGCATTG
 ATTCCCATTCAATCTCATTCTGGATATGTTCAATTGAGTAAAGGAGGAGAGACCCCTATA
 CGCTATTAAATGTCCTTCTGGCTATCCCCCTTGGTCAATTAAAGCTAATGTAAGCACATCTA
 GAGGAAGGCGCAGCTCTCTGACGTAGATCATTAAAGCTAATGTAAGCACATCTA
 AGGGATAACATGATTAAAGGTTGAAATGGCTTGAATCATTGGTTGAGGGTGTGTTA
 TTTGAGTCATGAATGTACAAGCTCTGTAATCAGACCAGCTAAATACCCACACCTTT
 TCGTAGGTGGCTTCTCAGAGCTGGCTCATAACAAATAAGTTTGAAAGGCCA
 TGGCTTTCACACAGTTATTGACGTTATCTGAAAGCAGACTGTTAGGAGCAGT
 ATTGAGTGGCTGTCACACTTGAGGCAACTAAAAGGCTCAAACGTTGATCAGTTCTT
 TTCAGGAAACATTGTGCTCTAACAGTATGACTATTCTTCCCCACTCTAAACAGTGTGAT
 GTGTGTTATCCTAGGAAATGAGAGTTGGCAAACAACTCTCATTTGAATAGAGTTGTG
 TACTTCTCCATATTAAATTATGATAAAATAGGTGGGGAGAGTCTGAACCTAACTGTCA
 TGTTTGTGTTCATCTGTCAGCTAACAGTATTGAACTTTGAAAGCTGATGACGTTATTG
 CCAATTATGTTGTCACGTCACACTCATGTCAGGGCTGGAGACTCATTGATGATAAGAATA
 TTTCTGACAGTGAGTGACCCGGAGTCTGGTGTACCCCTCTACCAAGTCAGCTGCCTGCGAG
 CAGTCATTTCCTAAAGGTTACAAGTATTGAACTTTGAGTTGACTGACAGGCAAATGTC
 ATGAAGTTATTCTCTTAAACATGGTAGGAAAGCTGATGACGTTATTGATTTGTCTGGATT
 ATGTTCTGGAATAATTACAAAACAAGCTATTGAGTTGACTGACAGGCAAACAA
 TGACAGTGGATTCTCTTACAATGGAAAAAAATCCTATTGTAAATTAAAGGACTTCCC
 TTTTGTAACATAATCCTTTATTGGTAAAATTGTAAATTAAAGTGTCAACTTG

FIGURE 4

MSDIDGWFRSIPAI TRYWFAATVAVPLVGKLGLISPAYLFLWPEAFLYRFQIWRPITATFYF
PVGPGTGF LYLVNLYFLYQYSTRLETGAFDGRPADYLFMLLFNWICIVITGLAMDMQLLMIP
LIMSVLYVWAQLNRDMIVSFWGTRFKACYLPWVILGFNYIIGGSVINELIGNLVGHLYFFL
MFRYPMDLGGRNFLSTPQFLYRWLPSRRGGVSGFGVPPASMRRAADQNGGGGRHNWGQGFRL
GDQ

Transmembrane domain:

amino acids 98-116, 152-172

N-myristoylation site.

amino acids 89-95, 168-174, 176-182, 215-221, 221-227, 237-243

Glycosaminoglycan attachment site.

amino acids 218-222

FIGURE 5

GGGGCCGCGGTCTAGGGCGGCTACGTGTGCCATAGCGACCATTGCATTAACGGTTG
 GTAGCTTCTATCCTGGGGCTGAGCGACTGCAGCTCTCCCTACTCCCTCTCGGCT
 CCTTGTGGCCAAAGGCCTAACCGGGTCCGGCGGTCTGGCCTAGGGATCTTCCCCGTTGCC
 CCTTGGGCGGG**ATG**GCTGCGGAAGAAGAAGACGAGGTGGAGTAGGGTAGTGGAGAGCATCG
 CGGGGTTCCCTGCAGGGCCCAGACTGGTCCATCCCCATCTTGGACTTGTGGAACAGAAATGT
 GAAGTTAACTGCAAAGGAGGGCATGTGATAACTCCAGGAAGCCCAGAGCCGGTGATTTGGT
 GGCCTGTGTTCCCTTGTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGATT
 ATCAGGAATACAAGAACTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAATT
 AATGAAGATCAATTCAAGAACGATGCACCTCTCCTCTGCAAAGACCCATACATCACAGGC
 CATTGCAACCTGTGTTGGCAGCAGAAGATTTACTATCTTAAAGCAATGATGGTCCAGA
 AAAACATTGAAATGCAGCTGCAAGCCATTGAATAATTCAAGAGAGAAATGGTGTATTACCT
 GACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAAACACGAAGAGATGAAAATCCT
 GAGGGAAAGTTCTAGAAAATCAAAAGAGGAATATGACCAGGAAGAAGAAAGGAAGAGGAAAA
 AACAGTTATCAGAGGCTAAAACAGAACAGAGGCCACAGTCATCCAGTGAAAGCTGCAATAATG
 AATAATTCCAAGGGATGGTGAACATTGACACCCCACCCCTCAGAAGTTAAATGCATT
 TGCTAATCAGTCAATAGAACCTTGGAAAGAAAAGTGGAAAGGTCTGAAACTTCCTCCCTCC
 CACAAAAAGGCCTGAAGATTCTGGCTTAGAGCATGCGAGCATTGAAGGACCAATAGCAAAC
 TTATCAGTACTTGGAACAGAACGAGAACACTATCTCAAGCAGAACAGAGA
 TAAGTTGATGTCCATGAGAAAGGATATGAGGACTAAACAGATAAAATATGGAGCAGAAAG
 GAAAACCCACTGGGAGGTAGAGGAAATGACAGAGAAACCAGAAATGACAGCAGAGGAGAAG
 CAAACATTACTAAAGAGGAGATTGCTTGCAGAGAAACTCAAAGAAGAAGTTATTAATAAG**TA**
ATAATTAAAGAACAAATTAAACAAAATGGAAGTTCAAATTGTCTAAAAATAATTATTAGTC
 CTTACACTG

FIGURE 6

MAAEEEDEVEWVVESIAGFLRGPDWSIPILDVEQKCEVNCKGGHVITPGSPEPVILVACVP
LVFDDEEESKLTYTEIHQEYKELVEKLLEGYLKEIGINEDQFQEACTSPLAKTHTSQAILQP
VLAAEDFTIFKAMMVQKNIEMQLQAIRIIQERNGVLPDCLTDGSDVVSVDLEHEEMKILREVL
RKSKEEYDQEEERKRKKQLSEAKTEEPTVHSSEAAIMNNSQGDGEHFAHPPSEVKMHFANQS
IEPLGRKVERSETSSLPQKGLKIPGLEHASIEGPIANLSVLGTEELRQREHYLKQKRDKLMS
MRKDMRTKQIQNMEQKGKPTGEVEEMTEKPEMTAEKQTLLKRRLLAEKLKEEVINK

N-glycosylation sites.

amino acids 224-228, 246-250, 285-289

N-myristoylation site.

amino acids 273-279

Amidation site.

amino acids 252-256

Cytosolic fatty-acid binding proteins.

amino acids 78-108

FIGURE 7

GGGCACAGCACATGTGAAGTTTGATGATGAAGAAGAAAGCAAATTGACCTATAACAGAGAT
TCATCAGGAATACAAAGAACTAGTTGAAAAGCTGTAGAAGGTTACCTCAAAGAAATTGGAA
TTAATGAAGATCAATTCAAGAACGCATGCACCTCTCCTCTTGCAGAACCCATACATCACAG
GCCATTTGCAACCTGTGTTGGCAGCAGAAGATTTACTATCTTAAAGCAATGATGGTCC
AGAAAAACATTGAAATGCAGCTGCAAGCCATTGAATAATTCAAGAGAGAAATGGTGTATTA
CCTGACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAAT
CCTGAGGGAAAGTTCTTAGAAAATCAAAAGAGGAATATGACCAGGAA

FIGURE 8

GCGTGGTTTGTCTGCAATAGCGGGCTAGAGGGAGGGCTTTGCCTATAACCTACTG
 TAGCTTCTCCACGTATGGACCCCTAAAGGCTACTGCTGCTACTACGGGCTAGACAGTTACTG
 TCTCAGCTCTAGGATGTGCGTTCTCCACTAGAAGCTCTGAGGGAGGTAAATTAAAAAAC
 AGTGGAATGGAAAAACAGTGCTTAGTCATCCTGTAATATGCTCCTGTCAACAATGTATAC
 ATTCCTGCTAGGTGCCATATTCTATTGCTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATT
 CTGCCAATGAAGAAAACAAGTATGATTATCTCCAACACTGTGAATGTGTGCTCAGAACTG
 GTGAAGCTAGTTCTGTGCTTGTGATTCTGTGTTATAAGAAAGATCATCAAAGTAG
 AAATTGAAATATGCTCCTGGAAGGAATTCTGATTTCATGAAGTGGTCCATTCCCTGCCCT
 TTCTTATTCTGGATAACTTGATTGCTTCTATGTCCTGTCCTATCTCAACCAGCCATG
 GCTGTTATCTCTCAAATTCTAGCATTATAACAACAGCTCTCTATTCAAGGATAGTGCTGAA
 GAGCGCTAAACTGGATCCAGTGGCTTCCCTGACTTATTTGTCTATTGTCCT
 TGACTGCCGGACTAAAACCTTACAGCACAACCTGGCAGGACGTGGATTTCATCACGATGCC
 TTTTCAGCCCTCCAATTCTGCCTTCTTCAAGAGTGAGTGTCCCAGAAAAGACAATTG
 TACAGCAAAGGAATGGACTTTCTGAAGCTAAATGGAACACCACAGCCAGAGTTTCAGTC
 ACATCCGTCTGGCATGGGCATGTTCTATTATAGTCCAGTGTGTTATTCTCAATGGCT
 AATATCTATAATGAAAAGATACTGAAGGAGGGAAACCAGCTCACTGAAAGCATCTTCATACA
 GAACAGCAAACCTATTCTTGGCATTCTGTTAATGGCCTGACTCTGGCCTTCAGAGGA
 GTAACCGTGATCAGATTAAGAACGTGGATTTTTATGGCACAGTGCATTTCAGTAGCC
 CTTATTGTAACTGCATTCCAGGGCCTTCAGTGGCTTCATTCTGAAGTTCCTGGATAA
 CATGTTCCATGTCTGATGGCCAGGTTACCACTGTCAATTACACAAACAGTGTCTGTCCTGG
 TCTTGACTTCAGGCCCTCCCTGGAATTTCATTGGAAGCCCCATCAGTCCTCTCTATA
 TTTATTATAATGCCAGCAAGCCTCAAGTCCGAATACGCACCTAGGCAAGAAAGGATCCG
 AGATCTAAGTGGCAATCTTGGAGCGTCCAGTGGGATGGAGAAGAACTAGAAAGACTTA
 CCAAACCCAAGAGTGATGAGTCAGATGAAGATACTTCTAACTGGTACCCACATAGTTGCA
 GCTCTCTGAAACCTTATTTCACATTTCAGTGTGTAATATTATCTTTCACTTGATA
 AACCAGAAATGTTCTAAATCCTAATATTCTTGCAATATCTAGCTACTCCCTAAATGGTT
 CCATCCAAGGCTTAGAGTACCCAAAGGCTAAGAAATTCTAAAGAAACTGATAACAGGAGTAACA
 ATATGAAGAATTCTTAATATCTCAGTACTTGATAATCAGAAAGTTATATGTGCAGATTAT
 TTTCCCTGGCCTCAAGCTCCAAAAACTGTAATAATCATGTTAGCTATAGCTGTATAT
 ACACATAGAGATCAATTGCCAATATTACAATCATGTTAGTTCTAGTTACATGCCAAGT
 CTTCCCTTTAACATTATAAAAGCTAGGTTGTCTTGAAATTGAGGCCCTAGAGATAGT
 CATTTGCAAGTAAAGAGCAACGGGACCCCTCTAAAACGTTGGTTGAAGGACCTAAATAC
 CTGGCCATACCATAGATTGGGATGATGTTAGCTGTGCTAAATATTGCTGAAGAAGCAGT
 TTCTCAGACACACATCTCAGAATTAAATTAGAAATTGATGGGAAATTGGATTGGT
 AATAATCTTTGATGTTAAACATTGGTCCCTAGTCACCAGTAGTTACCACTGTATT
 AGTCATTAAACAAGCCACGGTGGGCTTTCTCCTCAGTTGAGGAGAAAATCTTGAT
 GTCATTACTCCTGAATTATTACATTGGAGAATAAGAGGGCATTATTATTAGTTACT
 ATTCAAGCTGTGACTATTGTTATCTTCAAGAGGTTGAAATGCTGGCTTCAGAATCATA
 CAGATTGTCAGTGAAGCTGATGCTAGGAACCTTAAAGGATCCTTCAAAAGGATCACTT
 AGCAACACATGTTGACTTTAACTGATGTTAGAATATTAAACTCTAAATAGAAAGACC
 AGTAATATATAAGTCACCTTACAGTGTACTTCACACTTAAAGTGCATGGTATTGTCATG
 GTATTGTCATGCCAGTTAACTCTCGTAGATAGAGAAGTCAGGTGATAGATGATATTAA
 AAATTAGCAAACAAAAGTGACTTGCTCAGGGTCATGCAGCTGGGTGATGATAGAAGAGTGGG
 CTTTAACTGGCAGGCCGTATGTTACAGACTACCATACTGTAATATGAGCTTATGGTGT
 CATTCTCAGAAACTTATACATTCTGCTCCTTCTCCTAAGTTCATGCGAGATGAATATA
 AGGTAATATAACTATTATATAATTGATTCACACAAATAATGACTGGCAAGAATTG
 GTGGAAATTGTAATTAAAATAATTAAACCT

FIGURE 9

MEKQCCSHPVICSLSTMYTFLLGAI FIALSSSRILLVKYSANEENKYDYLPTTVNVCSELVK
LVFCVLVSFCVIKKDHQSRNLKYASWKEFSDFMKWSIPAFLYFLDNLIVFYVLSYLPAMAV
IFSNFSIITTALLFRIVLKRRLNWIQWASLLTLFLSIVALTAGTKTLQHNLAGRGFHHDAFF
SPSNSCLLFRSECPRKDNCATAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVQCFISSLANI
YNEKILKEGNQLTESIFIQNSKLYFFGILFNGLQLQRSNRDQIKNCGFFYGHSAFSVALI
FVTAFQGLSVAFILKFLDNMFHVLMAQVTTVIITTVSVLVFDFRPSLEFFLEAPSVLLSIFI
YNASKPQVPEYAPRQERIRDLSGNLWERSSGDGEELERLTKPKSDESDEDTF

Transmembrane domains:

amino acids 16-36 (type II), 50-74, 147-168, 229-250, 271-293,
298-318, 328-368

N-glycosylation sites.

amino acids 128-132, 204-208, 218-222, 374-378

Glycosaminoglycan attachment site.

amino acids 402-406

N-myristoylation sites.

amino acids 257-263, 275-281, 280-286, 284-290, 317-323

FIGURE 10

CGTGCCTGCGCAATGGGTGTCGGTCCGCTTTCCAATCCGGACGTAATCGTGGTTTG
TTCTGCAATAGGCGGCTTAGAGGGAGGGCTTTCGCCTACCTACTGTAGCTCTCAC
GTATGGACCCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTGTCTCAGCTCTAG
GATGTGCGTTCTTCACTAGAACGCTTTCTGAGGGAGGTAATTAAAAAACAGTGAATGGAA
AACAGTGTGCTAGTCATCCTGTAATATGCTCCTGTCAACAATGTATACATTCTGCTAGG
TGCCATATTGCTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATTCTGCCAATGAAG
AAAACAAGTATGATTATCTTCCAACACTGTGAATGTGTGCTCAGAACTGGTGAAGCTAGTT
TTCTGTGTGCTTGTGCATTCTGTGTTATAAAGAAAGATCATCAAAGTAGAAATTGAAATA
TGCTTCCTGGAAGGAATTCTCTGATTCATGAAGTGGTCCATTCCCTGCCTTCTTATTCC
TGGATAACTTGATTGTCTTCTATGTCCTGTCCTATCTCAACCAGCCATGGCTGTTATCTTC
TCAAATTTAGCATTATAACAAACAGCTCTTCTATTCAAGGATAGTGCTGAAGAGGCGTCTAAA
CTGGATCCAGTGGCTTCCCTCCTGACTTATTGTCTATTGTGGCCTGACTGCCGGGA
CTAAAACCTTA

FIGURE 11

CGGACGC GTGGCGGACCGTGGCGGACGC GTGGGCCGGCTGGCTAGCGCGCGGCC
 GTGGCTAAGGCTGCTACGAAGCGAGCTGGGAGGAGCAGCGGCCTGCGGGGCAGAGGAGCAT
 CCCGTCTACCAGGTCCCAAGCGCGTGGCCCGCGGGTCA TGCCAAAGGAGAACGGCGCCGAG
 AGCGGCTCCCGCGCGGGCTGCTACCCACCAAGC ATCCCAAAGC ACTGAACGCCCGGCCA
 GGTGAAGAAAGAACGAAAAAGAAGAACACAACAGTTGTCTGTTGCAACAAGCTTGCTATG
 CACTTGGGGAGCCCCCTACCAAGGTGACGGCTGTGCCCTGGTTCTCCTCAGATCTAC
 CTATTGGATGTGGCTCAGGTGGCCCTTCTGCTCCATCATCCTGTTGTGGCCGAGC
 CTGGGATGCCATCACAGACCCCTGGTGGGCCTCTGCATCAGCAAATCCCCCTGGACCTGCC
 TGGGTCGCCTATGCCCTGGATCATCTTCTCCACGCCCTGCCGTATTGCCACTTCCTC
 ATCTGGTTCGTCCCAGCTTCCACACGGCCAGACCTATTGGTACCTGCTTTCTATTGCCCT
 CTTTGAACAAATGGTACGTGTTCCATGTTCCCTACTCGGCTCTCACCATGTCATCAGCA
 ACCGAGCAGACTGAGCGGGATTCTGCCACCGCCTATCGGATGACTGTGGAAGTGTGCTGGCAC
 AGTGTGGCACGGCGATCCAGGGACAAATCGTGGCCAAGCAGACACGCCTTGTTCAGG
 ACTTCAATAGCTCTACAGTAGCTTACAAAGTCCAACCATACACATGGCACCACTCACAC
 AGGGAAACGCAAAGGCATACCTGCTGGCAGCGGGGTCA TTGTCTGTATCTATATAATCTG
 TGCTGTCACTCTGATCCTGGCGTGCAGGAGCAGAGAGAACCTATGAAGGCCAGCAGTCTG
 AGCCAATGCCACTTCCGGGCCTACGGCTGGTCA TGAGCCACGCCATACATCAAACCT
 ATTACTGGCTCCCTTCA CCTCCTGGCTTCA TGCTGGTGGAGGGAACTTGTCTTGT
 TTGCACCTACACCTTGGCTTCCGCAATGAATTCCAGAATCTACTCCCTGGCATCATGCTCT
 CGGCCACTTAACCATTCCCATCTGGCAGTGGTCTTGACCCGGTTGGCAAGAAGACAGCT
 GTATATGTTGGGATCTCATCAGCAGTGCCTATCTCATCTGGTGGCCCTATGGAGAGTAA
 CCTCATCATTACATATGCCGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCCTTAC
 TACCCCTGGTCCATGCTGCCATGTCATTGACGACTTCCATCTGAAGCAGCCCACCTCCAT
 GGAACCGAGCCCATCTTCTCTCTATGTCTTCA CCAAGTTGCCTCTGGAGTGT
 ACTGGCATTCTACCCCTCAGTCTGGACTTTGCAGGGTACCAAGACCCGTGGCTCGCAGC
 CGGAACGTGTCAAGTTACACTGAACATGCTCGT GACCATGGCTCCCATAGTTCTCATCCTG
 CTGGCCTGCTGCTCTCAAAATGTACCCATTGATGAGGAGAGGCCAGAATAAGAA
 GCCCTGCAGGCACTGAGGGACGAGGCCAGCAGCTGGCTGCTCAGAAACAGACTCCACAG
 AGCTGGCTAGCATCCTCTAGGGCCGCCACGTTGCCGAAGCCACCATGCAGAACGCCACAG
 AAGGGATCAGGACCTGCTGCCGGCTTGCTGAGCAGCTGGACTGCAGGTGCTAGGAAGGGAA
 CTGAAGACTCAAGGAGGTGGCCAGGACACTTGCTGTGCTACTGTGGGCCGGCTGCTCTG
 TGGCCTCCTGCCTCCCCCTGCCCTGCCGTGGGCCAAGCCCTGGGCCACTGTGAATA
 TGCCAAGGACTGATGGGCCTAGCCCGAACACTAATGTAGAAACCTTTTACAGAGCC
 TAATTAATAACTTAATGACTGTGTCATAGCAATGTGTGTATGTATATGTCTGTGAGCTA
 TTAATGTTATTAATTTCATAAAAGCTGGAAAGC

FIGURE 12

MWLRWALSPPSSCLWAEPGMPSQTPWWASASANPPGPAWVALCPGSSSPRPWPSLPTSSSG
SCPTSHTARPIGTCFSIASLKQWSRVSMFPTRLSPCSSATEQTERDSATAYRMTVEVLGTVL
GTAIQGQIVGQADTPCFQDFNSSTVASQSANHTHGTTSHRETQKAYLLAAGVIVCIYIICAV
ILILGVREQREPYEAQQSEPIAYFRGLRLVMSHGPYIKLITGFLFTSLAFMLVEGNFVLFC
YTLGFRNEFQNLLLAIMSATLTIPIWQWFLTRFGKKTAVYVGIISSAVPFLILVALMESNLI
ITYAVAVAAGISVAAFLPWMSMLPDVIDDFHLKQPHFHGTEPIFFSFYVFFTAKFASGVSLG
ISTLSLD FAGYQTRGCSQPERVKFTLNMLVTMAPIVLILLGLLFKMYPIDEERRRQNKKAL
QALRDEASSSGCSETDTELASIL

FIGURE 13

GGGAAACGCAAAAGGCATACTGCTGGCAGCGGGGTATTGTCTGTATCTATATAATCTGT
GCTGTCATCCTGATCCTGGCGTGCAGGAGCAGAGAGAACCTATGAAGCCCAGCAGTCTGA
GCCAATCGCCTACTTCCGGGCCTACGGCTGGTATGCCACGGCCCATACATCAAACCTTA
TTACTGGCTTCCTCTTCACCTCCTGGCTTCATGCTGGTGGAGGGAACTTGTCTTGT
TGCACCTACACCTTGGGCTTCCGCAATGAATTCCAGAATCTACTCCTGCCATCATGCTCTC
GGCCACTTTAACCAATTCCCCTGGCAGTGGTCTTGACCCGGTTGGCAAGAAGACAGCTG
TATATGTTGGGATCTCATCAGCAGTGCCATTCTCATCTGGTGGCCCTCATGGAGAGTAAC
CTCATCATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTACT
ACCCTGGTCCATGCTGCCTGATGTCATTGACGACTTCCATCTGAAGCAGCCCCACTTCCATG
GAACCGAGCCCAT

FIGURE 14

GGGGCTCGGCCAGCGCTAGCGTAGTCGGCTGGTAAGGATTACAAAAGGTGCAGGT
ATGAGCAGGTCTGAAGACTAACATTGTGAAGTTGTAAAACAGAAAACCTGTAGAA**ATGT**
GGTGGTTTCAGCAAGGCCTCAGTTCCCTTCAGCCCTGTAAATTGGACATCTGCTGCT
TTCATATTCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTACCTTATAT
CAGTGACACTGGTACAGTAGCTCCAGAAAAATGCTTATTGGGCAATGCTAAATATTGCGG
CAGTTTATGCATTGCTACCATTATGTTGTTATAAGCAAGTTCATGCTCTGAGTCCTGAA
GAGAACGTTATCATCAAATTAAACAAGGCTGGCCTGTACTTGAATACTGAGTTGTTAGG
ACTTTCTATTGTGGCAAACCTCCAGAAAACAACCCCTTTGCTGCACATGTAAGTGGAGCTG
TGCTTACCTTGGTATGGCTCATTATATATGTTGTTCAGACCATCCTTCCTACCAAATG
CAGCCAAAATCCATGGCAAACAAGTCTCTGGATCAGACTGTTGGTTATCTGGTGTGG
AGTAAGTGCACTTAGCATGCTGACTTGCTCATCAGTTGCACAGTGGCAATTGGGACTG
ATTTAGAACAGAAACTCCATTGGAACCCGAGGACAAAGGTTATGTGCTTCACATGATCACT
ACTGCAGCAGAATGGTCTATGTCATTTCTTCTTGGTTTCTGACTTACATTGTA
TTTCAGAAAATTCTTACGGTGGAAAGCCAATTACATGGATTAACCCCTATGACACTG
CACCTGCCCTATTAACAATGAACGAACACGGCTACTTCCAGAGATATT**TGAT**GAAAGGAT
AAAATATTCTGTAATGATTATGATTCTCAGGGATTGGGAAAGGTTCACAGAAGTTGCTTA
TTCTCTGAAATTCAACCACTTAATCAAGGCTGACAGTAACACTGATGAATGCTGATA
ATCAGGAAACATGAAAGAACGCCATTGATAGATTATTCTAAAGGATATCATCAAGAAGACTA
TTAAAAACACCTATGCCTATACTTTTATCTCAGAAAATAAGTCAAAAGACTATG

FIGURE 15

MWWFQQGLSFLPSALVIWTSAAFIFSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNI
AAVLCIATIYVRYKQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTLFAAHVSG
AVLTFGMGSLYMFVQTILSYQMOPKIHGKQVFIRLLLVIWCGVSAWSMLTCSSVLHSGNFG
TDLEQKLHWNPEDKGYVLHMITTAAEWSMSFSFFGFFLTYIRDFQKISLRVEANLHGLTLYD
TAPCPINNERTRLLSRDI

FIGURE 16

CGGACGCTTGGGCNGGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGTGCCTGATGCCGAGT
TCCGTCTCTCGGGTCTTCTGGTCCCAGGCAAAGCGGAGCGGAGATCCTCAAACGGCCTA
GTGCTTCGCGCTTCCGGAGAAAATCAGCGGTCTAATTAAATTCTCTGGTTGTGAAGCAGT
TACCAAGAACATCTCAACCCTTCCCACAAAAGCTAATTGAGTACACGTTCTGTTGAGTACA
CGTTCCGTGATTACAAAAGGTGCAGGTATGAGCAGGTCTGAAGACTAACATTGAA
GTTGTAACAGAAAACCTGTTAGAAATGTGGTGGTTCAGCAAGGCCTCAGTTCCCT
TCAGCCCTTGTAATTGGACATCTGCTGCTTCATATTCATACATTACTGCAGTAACACT
CCACCATATAGACCCGGCTTACCTTATATCAGTGACACTGGTACAGTANC

FIGURE 17

CCCACGCGTCCGCCCGCCGTGCGTCCCAGTGCAAGTGAGCTTCGGCTGCCCGCGGG
 CGGGGGTGCAGGAGCCGACATGCGCCCGCTCTCGGCCTCCTCTGGTCTCGCCGGCTGCAC
 CTTCGCCTTGTACTTGCTGTCACGCGACTGCCCGCGGGAGACTGGGCTCCACCGAGG
 AGGCTGGAGGCAGGTCGCTGTGGTCCCCCTCGACCTGGCAGAGCTGCGGGAGCTCTGAG
 GTCCTCGAGAGTACCGGAAGGAGCACCAAGGCCTACGTGTTCTGCTCTTCTGCGGCGCTA
 CCTCTACAAACAGGGCTTGCCATCCCCGGCTCCAGCTTCTGAATGTTTAGCTGGTGCCT
 TGTTGGGCCATGGCTGGGCTTCTGCTGCTGTGTTGACCTCGGTGGTGCCACATGC
 TGCTACCTGCTCTCCAGTATTTGGCAAACAGTTGGTGGTGCCTACTTCCTGATAAAAGT
 GGCCCTGCTGCAGAGAAAGGTGGAGGAACAGAAACAGCTGTTTTCTTATTGTT
 TGAGACTTTCCCCATGACACCAAACGGTTCTTGAACCTCTGGCCCCAATTCTGAACATT
 CCCATCGTCAGTTCTCTCAGTTCTATGGTTGATCCCATAATTCTCATCTGTT
 GCAGACAGGGTCCATCCTGTAACCCCTAACCTCTGGATGCTTTCTCCTGGACACTG
 TCTTAAGCTGTTGCCATTGCCATGGTGCATTAATTCTGGAACCCTCATTAAAAATT
 AGTCAGAAACATCTGCAATTGAATGAAACAAGTACTGCTAATCATACACAGTAGAAAAGA
 CACATGACTGGATTTCTGTTGCCACATCCCTGGACTCAGTTGCTTATTGTGTAATGGA
 TGTGGCCTCTAAAGCCCTCATGGTTGATTGCCCTATAGGTGATGTGGACACTGTG
 CATCAATGTGCAGTGTCTTCAGAAAGGACACTCTGCTCTGAAGGTGATTACATCAGGT
 TTTCAAACCAGCCCTGGGTAGCAGACACTGCAACAGATGCCTCTAGAAAATGCTGTTGT
 GGCGGGCGCGGTGGCTACGCCGTAATCCAGCACTTGGGAGGCCGAGGCCGGTGATTC
 ACAAGGTCAGGAGTTCAAGACCAGCCTGGCCAAGATGGTGAATCCTGTCTAATAAAAAT
 ACAAAAATTAGCCAGGCGTGGTGGCAGGGTTGCAGTAAGCCAAGATCACACCACTGCACT
 AGGAGAATTGCTGAACCAAGGTGGCAGGGTTGCAGTAAGCCAAGATCACACCACTGCACT
 CCAGCCTGGGTGATAGAGTGAGACACTGTCTTGAC

FIGURE 18

MRPLLGLLVFAGCTFALYLLSTRLPRGRRLGSTEAGGRSLWFPSDLAELRELSEVLREYR
KEHQAYVFLFCGAYLYKQGFAIPGSSFLNVLAGALFGPWLGLLCVLTSGATCCYLSS
IFGKQLVSYFPDKVALLQRKVEENRNSLFFFLLFLRLFPMTPNWFLNLSAPILNIPIVQFF
FSVLIGLIPYNFICVQTGSILSTLTSDALFSWDTVKLLAIAMVALIPGTLIKKFSQKHLQ
LNETSTANHIHSRKDT

Important features:

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 101-123, 189-211

N-glycosylation sites.

amino acids 172-176, 250-254

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 240-244, 261-265

N-myristoylation site.

amino acids 13-19, 104-110, 115-121, 204-210

Amidation site.

amino acids 27-31

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 4-15

Protein splicing proteins.

amino acids 25-31

Sugar transport proteins.

amino acids 162-172

FIGURE 19

CCGAGGCAGGGAGGAGCCGAGGGGGCGCGAGCCCCCATGAATCATTGTAGTCATCAATT
 CCAGTTCTCAGCCGCTCAGTTGTGATCAAGGGACACGTGGTTCCGAACGCCAGCTCAGAA
 TAGGAAAATAACTGGGATTTATATTGGAAGACATGATCTTGCTGCCAACGAGATCAGCA
 TTTATGACAAACTTCAGAGACTGTTGATTGGTGGAGACAGACCGGCCATCAGTGTGGCATG
 TCAGAGAAGGCAATTGAAAAATTATCAGACAGCTGCTGGAAAAGAATGAACCTCAGAGACC
 CCCCCCGCAGTATCCTCTCCTTATAGTTGTGATAAGGTTCTCGAACCTTGGGATTAATCT
 TGCTCACTGCCTACTTGTGATTCAACCTTCAGCCCATTAGCACCTGAGCCAGTGCTTCT
 GGAGCTCACACCTGGCGCTCACTCATCACATTAGGCTGATGTCCTGCCATTGCCAA
 GAAGTACATGTCAGAAAATAAGGGAGTTCTCTGCATGGGGTGATGAAGACAGACCCCTTC
 CAGACTTTGACCCCTGGTGGACAAACGACTGTGAGCAGAATGAGTCAGAGCCCATTCTGCC
 AACTGCACTGGCTGTGCCAGAAACACCTGAAGGTGATGTCCTGGAAGACGCCAAGGAA
 ATTTGAGAGGCTCCATCCACTGGTGATCAAGACGGAAAGCCCCTGTTGGAGGAAGAGATTC
 AGCATTGGGCCAGTACCCCTGAGGCGACAGAAGGCTCTGAAGGGTTTCGCAAAG
 TGGTGGCGCTGTTCTGAGCGGTGGTCCCATTCCATTCCATGGAGGAGACCTCTGAA
 CAGATCACAAATGTTACGTGAGCTTTCTGTTCACTCACCTGCCATTCCAAAAGATG
 CCTCTTAAACAAGTGCTCTTCTCACCCAGAACCTGTTGGGGAGTAAGATGCATAAG
 ATGCCTGACCTATTTATCATTGGCAGCGGTGAGGCCATGTTGCAGCTCATCCCTCCCTCCA
 GTGCCGAAGACATTGTCAGTCTGTCAGGCCATGCCAATAGAGCCAGGGGATATCGGCTATGTCG
 ACACCAACCACTGGAAGGTCTACGTTAGCCAGAGGGGTCAGCCTTGGTCATCTGCGAT
 GGAACCGCTTCTCAGAACTGTAGAAATAGAACTGTGCACAGGAACAGCTCCAGAGCCGA
 AAACCAGGTTGAAAGGGAAAAATAAAACAAAAACGATGAAACTGCAAAAA

FIGURE 20

MDLAANEISIYDKLSETVDLVRQTGHQCGMSEKAIEKFIRQLLEKNEPQRPPPQYPLLIVVY
KVLATLGLILLTAYFVIQPFSPLAEPVLSGAHTWRSЛИHHIRLMSLPIAKKYMSENKGVPL
HGGDEDRPFPDFDPWWTNDC EQNESEPIPANCTGCAQKHLKVMLLEDAPRKFERLHPLVIKT
GKPLLEEEIQHFLCQYPEATEGFSEGFFAKWWRCFPERWFPPY PWRRPLNRSQMLRELFPV
FTHLPFPKDASLNKCSFLHPEPVVGSKMHKMPDLFIIGSGEAMLQLI PPPFQCRRHCQSVAMP
IEPGDIGYVDTTHWKVYVIARGVQPLVICDGTAFSEL

FIGURE 21

CCACGGTGTCCGTTCTCGCCCGGGCAGCTGTCCCCGAGGCAGGGAGGCCGAGGGGCG
CGAGCCCCGCATGAATCATTGTAGTCATCAATCATTCCAGTTCTCAGCCGTTCAGTTGTGATC
AAGGGACACGTGGTTCCGAACTGCCAGCTCAGAACATAGGAAAATAACTTGGGATTTATATT
GGAAGACATGGATCTTGCTGCCAACGAGATCAGCATTATGACAAACTTCAGAGACTGTTG
ATTTGGTGAGACAGACCGGCCATCAGTGTGGCATGTCAGAGAAGGCAATTGAAAAATTATC
AGACAGCTGCTGGAAAAGAACCTCAGAGACCCCCCCCAGTATCCTCTCCTTATAGT
TGTGTATAAGGTTCTCGAACCTGGGATTAATCTGCTCACTGCCTACTTGTGATTCAAC
CTTCAGCCCATTAGCACCTGAGCCAGTGCTTGTGGAGCTCAC

FIGURE 22

CCCACCGCGTCCGCCAACCGGTCCGGCTGAACACCTCTTGGAGTCAGCCACTGATGAGG
 CAGGGTCCCCACTTGCAGCTGCAGCAGCTGCAGCAGCTGCAGAGCGCTGCTCTGGCTGGTG
 CCACTGGTGCACGCTGCTAGACCGTGCCTATGAGCCCTGGGCTGCAGTGGGACTGCC
 CTCCCTGCCACCCACCAATGGCAGCCCCACCTCTTGAAGACTTCCAGGTTTTGTGCCA
 CACCCGAATGGCGCACTTCATCGACAAACAGGTACAGCCAACC**ATG**TCCCAGTTCGAAATG
 GACACGTATGCTAAGAGCCACGACCTTATGTCAGGTTCTGGAATGCTGCTATGACATGCT
 TATGAGCAGTGGGCAGCGGCCAGTGGGAGCGGCCAGAGTCGTCGGGCTTCCAGGAGC
 TGGTGTGGAACCTGCGCAGAGGGGGCGGCCCTGGAGGGCTACGCTACACGGCAGTGCTG
 AAGCAGCAGGCAACGCAGCACTCATGGCCCTGCTGCACTGGGGGCGCTGTGGCGCCAGCT
 CGCCAGCCATGTGGGCCTGGCGCTGAGGGACACTCCCATCCCCCTGGAAACTGTCCA
 GCGCCGAGACATATTACGCATGCGTCTGAAGCTGGTGCCTACAGCTACACGGGAGGAGC
 CTGGAAGCCAGCGCTCTCGAGACAATCTGGGTGAGGTTCCCTGACACCCACCGAGGAGG
 CTCACTGCCTCTGGCAGTGACCAAAGAGGCCAAAGTGAGCACCCCCACCGAGTTGCTGCA
 AGGACCAAGCTGGCGAGGACGAGCTGGCTGAGCTGGAGACCCGATGGAGGGAGCAGAACTG
 GATGAGCAGCGTGAGAAGCTGGTCTGTCGGCCGAGTGCAGCTGGTAGTGGCGCT
 GGTCCCAGGGCTGCTGGAGGTACCCACACAGAATGTATACTTCTACGATGGCAGCACTGAGC
 GCGTGGAAACCGAGGGCATGGCTATGATTCCGGCGCCACTGGCCAGCTGCGTGG
 GTCCACCTGCGCGTTCAACCTGCGCCGTTCAAGCTGGCAGCTTCTTATCGATCAGGC
 CAACTACTCCTCAACTCCCATGCAAGGGGGCACGACCCAGTCTCATCTCTAGCCAGA
 CTCCGAGACCCAGCCTGGCCCATCCCACCCATACCCAGGTACGAAACAGGTGTACTCG
 TGGCTCTGCGCCTACGGCCCCCTCTCAAGGCTACCTAACGAGCCGCTCCCCCAGGAGA
 GCTGCGTGCCTCAGGCCATTACCCAGAAATGGGTACAGCGTGAGATATCCAACCTCGAGTACT
 TGATGCAACTCAACACCATTCGCCCCGGACCTACAATGACCTGTCTCAGTACCCGTGTT
 CCCTGGGTCTGCAGGACTACGTGCCCCAACCTGGACCTCAGCAACCCAGCCGTCTCC
 GGACCTGCTAACGCCCCATCGGTGGTGAACCCAAAGCATGCCAGCTCGTAGGGAGAAGT
 ATGAAAGCTTGAGGACCCAGCAGGGACCATTGACAAGTTCACTATGGCACCCACTACTCC
 AATGCAGCAGCGTGTGACTACCTCATCCCGTGAGGCCCTCACCTCCCTGCACGTCCA
 GCTGCAAAGTGGCGCTTGACTGCTCCGACCGGCAGTCCACTCGGTGGCAGCCTGG
 AGGCACGCCTGGAGAGGCCCTGCCATGTGAAGGAGCTCATCCCGAATTCTTACTTTCT
 GACTTCTGGAGAACCGAACGGTTTGACCTGGGTGTCTCCAGTGAACAAACGAGAAGGT
 AGGCAGATGGGTGCTACCCCGTGGCCAGCTCTCGAGGACTTCACTACAGCAGCACGCC
 AGGCTCTGGAGTGGAGTATGTGCTGACACCTACAGAGTGGATGACCTCATTTGGC
 TACAAGCAGGGGGCCAGCGCGAGGAGGCCCTCAATGTTCTATTACTGCACCTATGA
 GGGGGCTGTAGACCTGGACCATGTGACAGATGAGCGGGAACCGAAGGCTCTGGAGGG
 CATTATCAGCAACTTTGGCAGACTCCCTGTCAGTGTGAAGGAGCCACATCCAAC
 GCTGAGGAAGCAGCCATCGCCTGCAACGCTGGACACTAACACTCACCTAGCATCT
 CCTGGACGAACCTCAAGGATTCTCGCAGAGGTGACTGTGAGTGCAGTGGCTGCT
 CCCACAGCTGGTTGCCCTATGACCGCAACATAAGCAACTACTTCAGCTCAGCAAAG
 ACCATGGGCAGCCACAAGACGCAGCGACTGCTGAGTGGCCGTGGGTGCCAGGCAGT
 GAGTGGACAAAGCACTGGCAGTGGCCCCGGATGGAAAGCTGCTATTAGCAGGCT
 ATGGCAGCCTGGGGTGACTGCACTACCCGTGGCAAGCTGGTGGCATCTACCTCAT
 CTTGATGTTAGTAACCTGCCCTGCACTGGACACCTGTGGCATCTACCTCATCT
 GGACACACAGTGTGATGGTGTGGCGCTCTGCATCAGGGTGGTGTGCACTAG
 CAGGCTGGCAGGACATGGGATGGGCTTCACTGGGCTTCACTGCCCT
 GAACTGACATGGCTGTTGACTGAGGATGGAACACTGTGATCATACACACTGTACGCC
 CGGACAGTTGTTAGCGGCACTACGGCCTCTGGGTGCCACATCCCTGGACCT
 TGGCATGGGTCCGAAGGCCAGATTGTGGTACAGAGCTCAGCGTGGGAACGT
 CAGGTACCTACTCCTGCACCTGTATTCACTGAATGGGAAGTTGCAGGCTTCACT
 GGCAGAGCAGCCTACAGCCCTGACGGTGACAGAGGACTTGTGTTGCTGG
 GCGCCCTGCACATCCTCAACTAAACACACTGCTCCGGCCGCCCTGGCC
 GTGGCATCCCGTGGCGTGGGAGCAAGGAGCGCAGCCACGTGCTGGTGG
 TGGCAAGCTCATCGTGGTGGTGCAGGAGCCAGCCCTGAGGTGCGCAG
 GAGCAGCCAGTGGGAGGAGACGGAATACAAC
 CCTACTGAGGCGCGCT**TGA**ACCTGGCCAGTCCGGCTGCTCGGG
 GCCCGGGAGGCCAGAAGTCGGCGGAACACCCCGGGGTGGGCAGGCC
 GCGGGGCCACCTGCCAGCTCAGGGATGGCGGGCGATGTTACCC
 CAGGGATTGGCG
 GCGGAAGTCCC
 GCCCCCTGCCGGCTGAGGGGCCAGCACTGGCGT

FIGURE 23

MSQFEMDTYAKSHDLMMSGFWNACYDMLMSSGQRQWERAQSRRAFQELVLEPAQRRARLEG
 RYTAVLKQQATQHSMALLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRLKLVPN
 HHFDPHLEASALRDNLGEVPLPTTEEASLPLAVTKEAKVSTPPELLQEDQLGEDELAETP
 MEAAELDEQREKLVLSAECQLVTVVAVVPGLLEVTTQNVFYDGSTERVETEEGIGYDFRRP
 LAQLREVHLRRFNLRRSALELFFIDQANYFLNFPCKVGTPVSSPSQTPRPQPGPIPHTQV
 RNQVYSWLLRLRPPSQGYLSSRSPQEMLRASGLTQKWVQREISNFEYLMQLNTIAGRKYNDL
 SQYPVFPWVLQDYVSPTLDLSNPAYFRDLASKPIGVVNPKHAQLVREKYESFEDPAGTIDKFH
 YGTHYSNAAGVMHYLIRVEPFTSLHVQLQSGRFDCSDRQFHSAAAWQARLESPADVKEIP
 EFFYFPDFLENQNGFDLGCLQLTNEKVDVVLPPWASSPEDFIQQHRQALESEYVSAHLHEW
 IDLIFGYKORGPAEEEALNVFYCTYEGAVDLDHVTDERERKALEGIISNFGQTPCQLLKEP
 HPTRLSAEEAAHRLARLDTNSPSIFQHDELKAFFAEVTVSASGLLGTHSWLPYDRNISNYF
 SFSKDPTMGSHKTQRLLSGPWPGSGVSGQALAVAPDGKLLFSGGHWDGSLRVTALPRGKLL
 SQLSCHLDVVTCLALDTCGIYLISGSRDTTCMVWRLHQGGLSVGLAPKPVQVLYGHGAAVS
 CVAISTELDMAVSGSEDTVIIHTVRRGQFVAALRPLGATFPGPPIFHLAGSEGQIVVQSSA
 WERPGAQVTYSLHLYSVNGKLRLAELAEQPTALTVDFTVLLGTAQCALHILQLNTLLPAA
 PPLPMKVAIRSVAVTKERSHVLVGLLEDGKLIIVVAGQPSEVRSSQFARKLWRSSRRISQVSS
 GETEYNPTEAR

N-glycosylation site.

amino acids 677-681

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 985-989

Tyrosine kinase phosphorylation site.

amino acids 56-65, 367-376, 543-551

N-myristoylation site.amino acids 61-67, 436-442, 604-610, 610-616, 664-670, 691-697,
 706-712, 711-717, 769-775, 785-791, 802-808, 820-826, 834-840,
 873-879, 912-918, 954-960

FIGURE 24

CGGACGCGTGGCGGACCGTGGGGCTGTGAGAAAGTGCAATAAATACATCATGCAACCC
 CACGGCCCACCTGTGAACTCCTCGTGCCAGGGCTGATGTGCGTCTCCAGGGCTACTCAT
 CCAAAGGCCTAATCCAACGTTCTGTCTCAATCTGCAAATCTATGGGGCCTGGGGCTCTTC
 TGGACCCTTAACGGTACTGCCCTGGCCAATGCGTCCTCGCTGGAGCCTTGCCTCCTT
 CTACTGGGCCTTCCACAAGCCCCAGGACATCCCTACCTCCCTTAATCTCTGCCTTCATCC
 GCACACTCCGTTACCACACTGGTCATTGGCATTGGAGGCCCTCATCCTGACCCTGTGCAG
 ATAGCCCAGGTACATGGAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCCGTAGC
 CCGCTGCATCATGTGCTGTTCAAGTGCTGCCCTGGTGTGGAAAAATTATCAAGTTC
 TAAACCGCAATGCATACATCATGATGCCATCTACGGGAAGAATTCTGTGTCTGCCAAA
 AATGCGTTCATGCTACTCATGCGAACATTGTCAGGGTGGCGTCTGGACAAAGTCACAGA
 CCTGCTGTTCTTGGGAAGCTGCTGGTGGCGAGGCGTGGGGCTGTCCCTTT
 TTTCTCCGGTCGCATCCGGGGCTGGTAAAGACTTAAGAGCCCCACCTCAACTATTAC
 TGGCTGCCCATCATGACCTCCATCCTGGGGCCTATGTCATGCCAGCGCTTCTCAGCGT
 TTTCGGCATGTGTGGACACGCTTCTGCTTGGAAAGACCTGGAGCGAACACAG
 GCTCCCTGGACCGGCCCTACTACATGTCCAAGAGCCTCTAAAGATTCTGGCAAGAAC
 GAGGCAGCCCCGGACAACAAGAAGAGGAAGTGACAGCTCCGGCCCTGATCCAGGACTGC
 ACCCCACCCCCACCGTCCAGCCATCCAACCTCACTTCGCTTACAGGTCTCCATTGTTGGT
 AAAAAAAAGTTTAGGCCAGGCGCCGTGGCTCACGCCGTAAATCCAACACTTGGAGAGGCTG
 AGGCAGGGCGGATCACCTGAGTCAGGAGTTGAGACAGCCTGGCCAACATGGTGAACCTCC
 GTCTCTATTAAAAATACAAAAATTAGCCGAGAGTGGTGGCATGCACCTGTCTCCCAGCTAC
 TCGGGAGGCTGAGGCAGGAGAATCGCTGAACCCGGGAGGCAGAGGTTGCAGTGAGCCGAGA
 TCGCGCCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAACAA
 AAAGATTTATTAAAGATATTGTTAACTC

FIGURE 25

RTRGRTRGGCEKVPINTSCNPTAHLVNSSCPGLMCVFQGYSSKG LIQR SVFNLQIYGV LGF
WTLNWVLALGQC VLAGAFASFYWAFHKPQDIPTFPLISAFIRTLRYHTGSLA FGALILT LVQ
IARVILEYIDHKL RGVQN PVARCIMCCFKCCLW CLEKF IFLRNAYIMIAIYGKNFCVSAK
NAFMLLMRNIVRVVVLDKVTDL LFFGKLLVVGGVGVL SFFFSGRIPGLGKDFKSPHLNYY
WLPI MTSILGAYVIASGFFSVFGMCVDTLFLCFLEDLERNN GSLDRPY YMSK SLLKILGKKN
EAPPDNKKRKK

FIGURE 26

GAGTCTTGACGCCGCCGGCTTGGTACCTCAGCGGAGCGCCAGGCCTCGGCCGT
 GGCTATGTTCGTGTCCGATTCCGAAAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCC
 TTCTCTCGTGGCCTCGGACGTGGATGCTCTGTGTGCGTGCAAGATCCTCAGGCCTTGTTC
 CAGTGTGACCACGTGCAATATAACGCTGGTCCAGTTCTGGTGGCAAGAACTTGAAACTG
 ATTTCTTGAGCATAAAGAACAGTTTATTCTCATAAACTGTGGAGCTAATGTAG
 ACCTATTGGATATTCTTCAACCTGATGAAGACACTATATTCTTGATGTGACTCCCATTAGG
 CCAGTCATGTGCAATGTATAAACGATAACCCAGATCAAATTACTCATAAACAAGATGA
 TGACCTTGAAGTTCCCGCTATGAAGACATCTCAGGGATGAAGAGGAGGATGAAGAGCATT
 CAGGAAATGACAGTGATGGTCAGAGCCTCTGAGAACGCGCACACGGTTAGAAGAGGAGATA
 GTGGAGCAAACCATGCGGAGGAGGCAGCGCGAGAGTGGAGGCCCCGAGAACAGAGACATCCT
 CTTTGACTACGAGCAGTATGAATATCATGGACATCGTCAGCCATGGTATGTTGAGCTGG
 CTTGGATGCTGCCAGGACCTGAATGACATGCTGTGGTGGCCATCGTGGACTAACAGAC
 CAGTGGTGCAAGACAAGATCACTCAAATGAAATACGTGACTGATGTTGGTGCAGCG
 CCACGTTCCCGCCACAACCACCGAACGAGGATGAGGAGAACACACTCTCCGTGGACTGCA
 CACGGATCTCCTTGAGTATGACCTCCGCCTGGTGCCTACAGCACTGGCCCTCCATGAC
 AGCCTGTGCAACACCAGCTACCGCAGCCAGGTTCAAGCTGTGGTGTGCATGGACAGAA
 GCGGCTCCAGGAGTTCTGCAGACATGGTCTTCCCTGAAGCAGGTGAAGCAGAACAGTCC
 AGGCCATGGACATCTCCTGAAGGAGAATTGCGGGAAATGATTGAAGAGTCTGCAAATAAA
 TTTGGGATGAAGGACATGCGGTGCAGACTTCAGCATTCTGGTCAAGCACAAGTT
 TCTGGCCAGCGACGTGGCTTGCACCATGTCTTGATGGAGAGCCCCGAGAACAGGATGGCT
 CAGGGACAGATCACTCATCCAGGCTCTGGACAGCCTCTCCAGGAGTAACCTGGACAAGCTG
 TACCATGGCCTGGAACCTGCCAAGAACGAGCAGCTGCGAGCCACCCAGCAGACCATTGCCAGCTG
 CTTGCACCAACCTCGTCATCTCCAGGGCCTTCTGTACTGCTCTCATGGAGGGCAC
 TCCAGATGTCTGCTGTTCTAGGCCGGCATCCCTAAGCCTGCTCAGCAAACACCTGCTCA
 AGTCCTTGTGTTGACAAAGAACCGGGCTGCAAACAGTGTGCCCCCTGGTATGGCTGCC
 CCCCTGAGCATGGAGCATGGCACAGTGACCGTGGTGGCATCCCCCAGAGACCGACAGCTC
 GGACAGGAAGAACTTTTGGAGGGCGTTGAGAAGGCAGCGGAAAGCACCAGCTCCCGA
 TGCTGCACAACCATTGACCTCTCAGTAATTGAGCTGAAAGCTGAGGATGGAGCAAGTT
 CTGGACGCACCTATTCCCTCTGTCCTAGGAATTGATTCTCCAGAAATGACCTTATT
 TATGTAACTGGCTTCATTAGATTGTAAGTTATGGACATGATTGAGATGTAGAACCCATT
 TTTTATTAAATAAAATGCTTATTAGGAAA

FIGURE 27

MFVSDFRKEFYEVVQSRVLLFVASDVLCAACKILQALFQCDHVQYTLVPVSGWQELETAF
LEHKEQFHYSILINCGANVDLLDILQPDDETIFFVCDSHRPVVNVYNDTQIKLLIKQDDD
LEVPAYEDIFRDEEEDEEHSGNDSDGSEPSEKRTRLEEEIVEQTMRRQRREWEARRDILF
DYEQYEHGTSSAMVMFELAWMLSKDLNDMLWWAIVGLTDQWVQDKITQMKYVTDVGVLQRH
VSRHNHRNEDEENTLSVDCTRISFEYDLRLVLYQHWSLHDSDLNTSYTAARFKLWSVHGQKR
LQEFLADMGLPLKQVKQKFQAMDISLKENLREMIEESANKFGMKDMRVQTFSIHFGFKHKFL
ASDVVFATMSLMESPEKDGSGTDHFIQALDSLRSNLDKLYHGLELAKKQLRATQQTIASCL
CTNLVISQGPFLYCSLMEGTPDVMLFSRPASLSLLSKHLLKSFVCSTKNRRCKLLPLVMAAP
LSMEHGTVTVVGIPPETDSSDRKNFFGRAFEKAAESTSSRMLHNHFDSLVIELKAEDRSKFL
DALISLLS

FIGURE 28

GTACCTCAGCGCGAGCGCCAGGCGTCCGGCCCGTGGCTATGNTCGTGTCCGATTCCGCA
AAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCCTCTCTCGTGGCCTCGGANGTGGAT
GCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTCCAGTGTGACCANGTGCAATATANGCT
GGTTCCAGTTCTGGGTGGCAAGAACTTGAAACTGCATTCTGAGCATAAAGAACAGTTTC
ATTATTATTCTCATAAACTGTGGAGCTAATGTAGACCTATTGGATATTCTTCAACCTGAT
GAAGACACTATATTCTTGTGTGACACCCATAGGCCAGTCAATGTTGTCAATGTATACAA
CGATACCC

FIGURE 29

CGAGGAACCCCTCTTTGGGTCTGGATTGGGACCCCTTCCAGTACCATTTTTCTAGTGAAC
CACGAAGGGACGATACCAGAAAACACCCCTCAACCCAAAGGAAATAGACTACAGCCCCAATTG
GCTGACTTTGGCTATAGAAAAAAGAAAGGAACGAAAAGAGACAGTTTTGGAAAGCTAA
GTCTCCCTTATCGAGTCAGAAACCCCCCTTCTGAGCTATTACAGCTTTAACATT
GAGTAAAGTACGCTCCGGTCAACC**ATG**GTGACAGCCGCCCTGGGTCCCGTCTGGCAGCGCTC
CTGCTCTTCTCTGATGTGAGATCCGTATGGTGGAGCTCACCTTGACAGAGCTGTGGC
CAGCGCTGCCAACGGTGTGACTCTGAGGACCCCTGGATCCTGCCCATGTATCCTCAG
CCTCTCCTCCGGCCGCCACGCCCTGCCAGATCACATTAAATCACCATC
CTGAAGGGTGACAAAGGGGACCCAGGCCAATGGGCCCTGCCAGGGTACATGGGCAGGGAGGG
TCCCCAAGGGGAGGCTGGCCCTCAGGGCAGCAAGGGTACAAGGGGAGATGGGCAGGCCCG
GCGCCCGTGCAGAACGCGCTTCAGGCCCTCAGTGGGCCAGAAGACGCCCTGCACAGC
GGCGAGGACTTCCAGACGCTCTCGAAAGGGTCTTGTGAACCTTGATGGTGCTTGA
CATGGGACCGGCCAGTTGCTGCTCCCCCTGCGTGGCATCTACTTCTTCAGCCTCAATGTGC
ACAGCTGGAATTACAAGGAGACGTACGTGACATTATGCATAACCAGAAAGAGGCTGTACATC
CTGTACGCGCAGCCCAGCGAGCGCAGCATCATGAGGCCAGAGTGTGATGCTGGACCTGGC
CTACGGGACCGCGTCTGGGTGCGGCTCTCAAGGCCAGCGCAGAACGCCATCACAGCA
ACGACTTCGACACCTACATCACCTCAGCGGCCACCTCATCAAGGCCAGGACGACT**TGA**GGG
CCTCTGGGCCACCCCTCCGGTGGAGAGGCTCAGGTGCTGGTCCCGTCCCTGCAGGGCTCAG
TTTGCACTGCTGTGAAGCAGGAAGGCCAGGGAGGTTCCCGGGGACCTGGCATCTGGGAGGA
CCCTGCTTCTATCTTGGCTGCCATCATCCCTCCCAGCTATTCTGCTCTCTCTCT
TGGACCTATTAAAGAAGCTTGTCAACCTAAATATTCTAGAACACTTCCAGCTCGTAGCCC
AGCACCTCTCAAACATTGAAATGCATGCCAATCACCCGGGTTCTGTGTTAAATGCAAGATTCT
GAECTCAGCAGGCTGAGTGGGTCAGGATTCTGTGTTCTCATATGTCCTGGGTGATGCTG
ATGGGGTCAGTCTATGAACCACACTGGAGCAACCAGGTTCTAGGACTTCTCAATATTCTAG
TACTTCTGAACATTCTGGAATTCCTCCCCACATTCTAGAATTCTCCAACATTTTTTTCT
TGAGACAGAGTCTTGTCTGTTGCCAGGCTAGAGTGCAGTGGTGCAATCTCAGTTACTGC
AACCTCTGCCTCCGGGTTCAAGCGATTCTCTGCCAGCTCCCTAGTGGTGGGATTAC
AGGCCTGCTACCATGCCCTGGTAATTGGTATTAGTAGAGATGGGGTTCACCAT
TTGGCCAGGCTGGTCTTGAACTCCTGACTCAGGTGACCCACCCGCCTGGCCTCTCAAAAT
GCTGGGATTACAGGTGTGAGCCACCGTGGCAATTCAACATTCTAAATTCTCTCAT
CCCTCCAGGGCTCCCCGTGCTATGTTCTTACCCCTTCCCCCTCTCTCTGTGCTCAGGCC
TGCACCACTGCAGCCACCGTTCTTATTCAATTAAACACTGAGCACTCACTCTGTGCT
GGGTCCCGGGAAAGGGTGAAGGGGGTCAAGACACAGGCCCTGCCCTCAGTGAAGGCA
GTCCAGGCCAGGGGGAGAGATGTGATAGGTTAAAGCAGACCCAGAGCTCATGGGG
GCCTGTGTTCTGGGTGTCAGGTGCTGCTGGTCTCCATTACCCACTGCTCCCCAAGGCTGG
TGGGACGGGGTCCGGTGGCAGGGGCAGGTATCTCCTCCGTTCTCATCCACCTGCCAG
TGCTCATCGTTACGAAACCCCAGGGGGCCTGGCCAGGTCAAGGGTTCTGTGAGGAGAGG
ACCCAGGAGTGTGGGGCATTGGGGGGTGAAGTGGCCCCGAAGAATGGAACCCACACCCA
TAGCTCTCCCCACAGCTGATACGGCATCCTGCGAGAAGACCTGCCCTCCTCACTGGGATCCC
CTTCCCTGCCTCTCCCCAGGGCTGCGAGGGCCTGCTCAGTCCCTTCCACCAAAGTCATCT
GAACCTCCGTTCTCCCCAGGGCCTCCAGCTGCCCTCAGACACTGATGTCTGCCCCAGGTGCT
CTCTGCCCTCATGCCCTCTCACCGGCCAGTGGCCCTCAGTCCAGGTTATCAAGGTG
CTAAGGGCCGGTGGGAGCAGTCTCGTCAGAGGCCCTCTCCGGCTGGTGTGCTGCCTTAC
AAACACCTGCAGGAGAAGGGCAACGGAAAGGCCCAAGGGCTTAAAGGCCCTCAGCAGGTCTGGGG
AGCTAGAGCAAAGGAGGGACCTCAGGGCTTCCGTTCTTCCAGGGTGGGGTGGCCTGGT
GTTCCCTAGCCTTCCAAACCCAGGTGGGCTGCCCTCTCCCAAGGGAGGGAGGGCAGGCC
CCATTGGTGCTCATGCAGACTCTGGGCTGAGGTGCCCCGGGGGTGATCTGGTGTGCTCAC
AGCCGAGGGAGCCGTGGCTCATGGCCAGATGACGGAAACAGGGTCTGACCAAGTGCCAGGA
AGACCTGTGCTATAAACCAACCTGCCATGGCCAGATGACGGAAACAGGGTCTGACCAAGTGCCAGGA
GTCCAGCATGATTAAAGAATGCTGTCTCTTGGAAAAAAAAAAAAAA

FIGURE 30

MVTAALGPVWAALLFLLMCEIRMVELTFDRAVASGCQRCCDSEDPLDPAHVSSASSSGRPH
ALPEIRPYINITILKGDKDPGPMGLPGYMGREGPQGEPGPQGSKGDKGEMGSPGAPCQKRF
FAFSVGRKTALHSGEDFQTLLFERVFVNLDGCFDMATGQFAAPLRGIYFFSLNVHSWNYKET
YVHIMHNQKEAVILYAQPSERSIMQSQSVMMLAYGDRVWVRLFKRQRENAIYSNDFDTYIT
FSGHLIKAEDD

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 72-75

C1q domain proteins.

amino acids 144-178, 78-111 and 84-117

FIGURE 31

ACTCGAACGCAGTTGCTCGGGACCAGGACCCCCCTCGGGCCCGACCCGCCAGGAAAGACTG
AGGCCGCGGCTGCCCGCCGGCTCCCTGCGCCTGCGCTGCTACTGCCCTGGGCCTGGGTGCAGG
CTCCAGGGTCCCTCTGCTGCGCTGCTACTGCCCTGGGCCTGGGTGCAGGAAAGAAGATGTG
GCTGCCCATCCGGCTGCCAGTCAGGCCAGCACAGACAGTCTCTGCACTGCCCGCCAGGGG
ACCACGGTCCCCGAGACGTGCCACCCGACACGGTGGGCTGTACGCTTTGAGAACGGCAT
CACCATGCTCGACGCAGGCAGCTTGCCGGCTGCCGGCTGCAGCTCCTGGACCTGTCAC
AGAACACAGATGCCAGCCTGCCAGCAGGGTCTCCAGCCACTGCCAACCTCAGAACCTG
GACCTGACGGCCAACAGGCTGCATGAAATACCAATGAGAACCTCCGGCTGGCCTGCCACAGC
CGAGCGCCTCTACCTGGCAAGAACCGCATCGGCCACATCCAGCCTGGTGCCTCGACACGC
TCGACCGCCTCTGGAGCTCAAGCTGCAGGACAACGAGCTGCAGGGCACTGCCCGCTGCC
CTGCCCCGCTGCTGCTGGACCTCAGCCACAACAGCCTCTGGCCCTGGAGGCCGGCAT
CCTGGACACTGCCAACGTGGAGGCCTGCGCAACCTCCACGACCTGGATGTGTCGACAAACAGCTGGAGC
AGGGGCTCTCAGCCGCTGCGCAACCTCCACGACCTGGATGTGTCGACAAACAGCTGGAGC
CGAGTGCCACCTGTGATCCAGGGCTCCGGGCTGACGCCCTGCCCTGAGGAGCTGGATG
CCGCATTGCCAGCTGCCGGCGAGGACCTGCCGGCTGGCTGCCCTGAGGAGCTGGATG
TGAGCAACCTAACGCTGCAGGCCCTGCCTGGCACCTCTGGCCCTCTCCCCCGCTGCC
CTGCTGGCAGCTGCCGCAACCCCTCAACTGCGTGTGCCCTGAGCTGGTTGGCCCTG
GGTGGCGAGAGCCACGTCACACTGCCAGCCCTGAGGAGACGCGCTGCCACTCCCAGCCA
AGAACGCTGGCGGCTGCTCCTGGAGCTTGAACAGCCGACTTGGCTGCCAGCCACC
ACCACAGCCACAGTGCCACCAACGAGGCCGTGGTGCAGGAGCCCACAGCCTGTCTTAG
CTTGGCTCCTACCTGGCTAGCCCCACAGGCCGGCACTGAGGCCCCAGGCCAC
CTGCCCAACCGACTGTAGGGCTGTCCCCAGGCCACTGAGGCCCCAGGCCAC
AATGGGGCACATGCCACCTGGGACACGGCACCACTGGCGTGTGTCGCCCCGAAGGTT
CACGGCCTGTACTGTGAGAGCCAGATGGGAGGGCACGCCAGCCCTACACCAAGTC
CGCCGAGGCCACCACGGCTGCCCTGACCCCTGGCATCGAGCCGTGAGCCCCAC
CTGGGCTGAGCGTACCTCCAGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTAC
TCGCAACCTATCGGCCCTGATAAGCGGCTGGTGCAGCTGCACTGCCCTGCC
AGTACACGGTACCCAGCTGCCGGCAACGCCACTTACTCCGTCTGTGTCATGCC
CCCCGGCGGGTGCCGGAGGGCGAGGAGGCCCTGCCGGGAGGCCATAC
CTCCAACCACGCCCAAGTCACCCAGGCCGAGGGCAACCTGCCCTGCC
CCCTGGCGCGGTGCTCTGGCCCGCTGGCTGCCGTGGGGCAGCCTACTGTG
GGCGGGCCATGGCAGCAGCGGCTCAGGACAAAGGGCAGGGGGCCAGGGGCTGG
GGAACCTGGAGGGAGTGAAGGTCCCTGGAGGCCAGGCCGAAGGCAACAGAGGGCG
AGGCCCTGCCAGCGGGCTGAGTGTGAGGTGCCACTCATGGCTTCCAGGGC
CAGTCACCCCTCCACGCAAAGCCCTACATCTAAAGCCAGAGAGAG
GGCTCTCAGCCAGTGAAGATGGCCAGCCCCCTGCCACACCAC
CAACCTGGGGATGTGTCAGACAGGGCTGTGACCACTGCCCTGCC
CCTCGGTCTCCCATCTGTGAGATGCTGCCAGCTGAGGCC
CGAGTGCCTATGAGGACAGTGTGCCCTGCCCTCGCAAC
GGCCCTGCCATGTGCTGGTAACGCATGCCCTGGCTCTG
GCCCTGGGGCCAGTGAAGGAAGCTCCGGAAAGAGCAGAGGGAGAG
TGACTCTAGTCTGGCCCCAGGAAGCGAAGGAACAAAAG
GGAACATGTTTGCTTTAAATATATATTATAAGAGAT
GGAAGATGTTTCAAACCTCAGAGACAAGGACTTGG
AAGGCCTTTGTAAGAAAAAATAAAAGATGAAGTGTGAA

FIGURE 32

MCSRVPLLLPLLLALGPGVQGCPSCQCSQPQTVFCTARQGTTPRDVPPDTVGLYVFEN
GITMLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETFRGLR
RLERLYLGKNRIRHIQPGAFDTLDRLLELKQDNEILRALPPLRLPRLLLLDLSHNSLLALEP
GILDGTANVEALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRGLTRLRLAG
NTRIAQLRPEDLAGLAALQELDVSNLSQLALPGDLSGLFPRLLAARNPFCNCVCPPLSWFG
PWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTATVPTTRPVVREPTALS
SSLAPTWLSPTAPATEAPSPPSTAPPTVGPPQDCPPSTCLNGGTCHLGTRHHLACLCPE
GFTGLYCESQMGQGTRPSPTPVTPRPPRSLTGIEPVSPTSLRVGLQRYLQGSSVQLRSI RL
TYRNLSGPDKRLVTLRLPASLAEYVTQLRPNATYSVCVMPLGPGRVPEGEAACGEAHTPPA
VHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAQDKGQVGPAG
PLELEGVKVPLEPGPKATEGGEALPSGSECEVPLMGFPGPGLQSPLHAKPYI

FIGURE 33

GAATCATCCACGCACCTGCAGCTCTGCTGAGAGAGTGCAAGCCGTGGGGTTTGAGCTCAT
 CTTCATCATTATGAGGAATAAGTGGAAAATCCTGGAAATACA**ATG**GAGACTCATCAG
 AAACATTTACATATTTGTAGTATTGTATGACAGCAGAGGGTATGCTCCAGAGCTGCCAG
 AAGAAAGGGAACTGATGACCAACTGCTCCAACATGTCTAAGAAAGGTTCCCGCAGACTTG
 ACCCCAGCCACACGACACTGGATTATCTATAACCTCCTTTCAACTCCAGAGTTCAA
 TTTCATCTGCTCCAAACTGAGAGTTTGATTCTATGCCATAACAGAATTCAACAGCTGG
 ATCTCAAAACCTTGAATTCAACAAGGAGTTAAGATTTAGATTTGCTAATAACAGACTG
 AAGAGTGAACTTGTGATTACTGGCAGGTCTCAGGTTATGATCTTCTTTAATGACTT
 TGACACCATGCCATCTGTGAGGAAGCTGGCAACATGTACACCTGGAAATCCTAGGTTGA
 GTGGGGCAAAATACAAAATCAGATTCCAGAAAATTGCTCATCTGCATCTAAATACTGTC
 TTCTTAGGATTCAAACATCTCCTCATTATGAGAAGGTTAGCCTGCCATCTAAACACAA
 AAAACTGCACATGTTTACCAATGGACACAAATTCTGGGTCTTGCATGATGGAATCA
 AGACTTCAAAATATTAGAAATGACAATATAGATGGCAAAAGCCAATTGTAAGTTATGAA
 ATGCAACGAAATCTAGTTAGAAAATGCTAAGACATCGGTTCTATTGCTTAATAAGTGA
 TTTACTCTGGGACGACCTTCTTCTTATCTTACAATTGTTGGCATACTCAGTGGAAACACT
 TTCAGATCCGAAATGTGACTTTGGTGGTAAGGCTTATCTGACCACAATTCTATTGACTAC
 TCAAATACTGTAATGAGAACTATAAAATTGGAGCATGTACATTTCAGAGTGTTCATCTCA
 ACAGGATAAAATCTATTGCTTTGACCAAAATGGACATAGAAAACCTGACAATATCAAATG
 CACAAATGCCACACATGCTTCTCCGAAATTACCTACGAAATTCCAAATATTAAATTGCCC
 AATAATATCTAACAGACAGGTTTAAAAGAACATCTCAACTGCCACTTGAAAACCTCT
 CATTTGAATGGCAATAAACACTGGAGACACTTCTTAGTAAGTTGCTTGCATAACAACAC
 CCTTGGAACACTGGATCTGAGTCAAAATCTATTACACATAAAATGATGAAAATTGCTCA
 TGGCCAGAAACTGTGGTCAATATGAAATCTGCATACAATAATTGTCATTCTGCTTCTCAG
 GTGCTTGCCAAAAGTATTCAAATACTTGACCTAAATAAAACCAATCCAAACTGTACCTA
 AAGAGACTATTCATCTGATGGCCTACGAGAACTAAATATTGCAATTAAATTCTAAACTGAT
 CTCCCTGGATGCAGTCATTTCAGTAGACTTCAGTTCTGAACATTGAAACTTCATCT
 CAGCCCATCTCTGGATTGTCAGAGCTGCCAGGAAGTTAAACTCTAAATGCCAGGAAAGAA
 ATCCATCCGGTGTACCTGTGAATTAAAAAATTCTCATCAGCTTGAAACATATTCAAGAGTC
 ATGATGGTTGGATGGTCAGATTACACCTGTGAATACCCCTTAAACCTAAGGGAAACTAG
 GTTAAAAGACGTCATCTCCACGAATTATCTTGCACACACAGCTCTGTTGATTGTCACCATTG
 TGGTATTATGCTAGTTCTGGGGTGGCTGTGGCCTCTGCTGTCTCAGTTGATCTGCC
 TGGTATCTCAGGATGCTAGGTCAATGCAACACAAACATGGCACAGGGTAGGAAAACAACCA
 AGAACAACTCAAGAGAAATGTCCGATTCCACGCATTATTCTCATACAGTGAACATGATTCTC
 TGTGGGTGAAGAACATGAAATTGATCCCCAATCTAGAGAAGGAAGATGGTCTATCTGATTG
 CTTTATGAAAGCTACTTGACCCCTGGCAAAAGCATTAGTGAAGAAATATTGTAAGCTTCATTG
 GAAAAGCTATAAGTCATCTTGTCTCCAACTTTGTCAGAATGAGTGGTGCCATT
 ATGAATTCTACTTGCACCCACAAATCTTCCATGAAAATTCTGATCATATAATTCTTATC
 TTACTGGAACCCATTCCATTCTATTGCATCCCACCCAGGTATCATAAAACTGAAAGCTCTC
 GGAAAAAAAAGCATACTTGAATGCCCAAGGATAGGCGTAATGTGGCTTCTGGGCAA
 ACCTTCGAGCTGCTTAAATGTTAGCCACAGAGAAATGATGAAACTGCAGACAA
 TTCACAGAGTTAAATGAAGAGTCTCGAGGTTCTACAAATCTCTGATGAGAACAGATTGCT
AT**TAA**AAATCCCACAGTCCTGGGAAGTGGGACACATACACTGTTGGGATGTACATTGATA
 CAACCTTATGATGGCAATTGACAATATTATTAAATAAAAATGGTTATCCCTCATA
 TCAGTTCTAGAAGGATTCTAAGAATGTATCCTATAGAAACACCTTCACAAGTTATAAGG
 GCTTATGAAAAAGGTGTTCATCCCAGGATTGTTATAATCATGAAAATGTGCCAGGTGC
 AGTGGCTCACTCTGTAATCCCAGCACTATGGGAGCCAAGGTGGGTGACCCACGAGGTCAA
 GAGATGGAGACCATCCTGGCAACATGGTAAACCCCTGTCTACTAAAAATACAAAAATT
 GCTGGCGTGTGGTGACGCCCTGTAGTCCAGCTACTTGGGAGGCTGAGGCAGGAGAAC
 CTTGAACCCGGGAGGTGGCAGTTGCAGTGAGCTGAGATCGAGCCACTGCACTCAGCCTGG
 GACAGAGCGAGACTCCATCTAAAAAGAAAAAGAAAAAGAAAAATGGAAAACATCC
 TCATGCCACAAATAAGGTCTATTCAATAATTATAGTACATTAAATGTAATATAATT
 CATGCCACTAAAAAGAATAAGGTAGCTGTATATTCTGGTATGGAAAAAACATATTAA
 GTTATAAAACTATTAGGTGGTGCAAAACTAATTGTTGGTTCTGCAATTGAAATGGCATTGAA
 ATAAAAGTGTAAAGAACATATACCCAGATGTAGTAACAGTGGTTGGGTCTGGGAGGTTGGA
 TTACAGGGAGCATTGATTCTATGTTGTATTCTATAATGTTGAATTGTTAGAATGA
 ATCTGTATTCTTTATAAGTAGAAAAAATAAGATAGTTTACAGCCT

FIGURE 34

MRLIRNIYIFCSIVMTAEGDAPELPEERELMTNCNSMSLRKVPADLTPATTLDLSYNLLFQ
LQSSDFHSVSKLRVLILCHNRIQQQLDLKTFEFNKELRYLDLSNNRLKSVTWYLLAGLRYLDL
SFNDFTMPICEEAGNMSHLEILGLSGAKIQKSDFQKIAHLHLNTVFLGFRTLPHYEEGSLP
ILNTTKLHIVLPMDTNFWVLLRDGIKTSKILEMTNIDGKSQFVSYEMQRNLSLENAKTSVLL
LNKVDLLWDDLFLLQFWHTSVEHFQIRNVTFGGKAYLDHNSFDYSNTVMRTIKLEHVHFR
VFYIQQDKIYLLLTKMDIENLTISNAQMPHMLFPNYPTKFQYLNFANNILTDELFKRTIQLP
HLKTLILNGNKLETLSLVSCFANNTPLEHLDLSQNLLQHKNDENCSPETVVNMNLSSYNKLS
DSVFRCLPKSIQILDNNNQIQTVPKETIHLMALRELNIAFNFLTDLPGCSHFSRLSVLNIE
MNFILSPSLDFVQSCQEVKTLNAGRNPFRCTCELKNFIQLETYSEVMMVGWSDSYTCEYPLN
LRGTRLKDVLHHELSCNTALLTIVVIMVLGLAVAFCCCLHFDLPWYLRMLGQCTQTWHRV
RKTTQEQLKRNVRFHAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESYFDPGKSISENI
VSFIEKSYKSIFVLSNFVQNEWCHYEFYFAHHNLFHENSDDIIILILLEPIPFYCIPTRYHK
LKALLEKKAYLEWPKDRRKCGFWANLRAAINVNVLATREMYELQFTTELNEESRGSTISLM
RTDCL

FIGURE 35

FIGURE 36

MSRPGTATPALALVLLAVTLAGVGAQGALEDPDYYGQEIWREPYYARPEPELETFSPPPLP
AGPGEEWERRPQEPRPPKRATKPKKAPKREKSAPEPPPGKHSNKKVMRTKSSEKAANDDHS
VRVAREDVRESCPPLGLETLKITDFQLHASTVKRYGLGAHRGRLNIQAGINENDFYDGAWCA
GRNDLQQWIEVDARRLTRFTGVITQGRNSILSDWVTSYKVMVSNDHTWVTVKNGSGDMIF
EGNSEKEIPVLNELPVPVMARYIRINPQSWFDNGSICMRMEILGCPLDPNNYYHRRNEMTT
TDDLDFKHHNYKEMRQLMKVVNEMCPNITRIYNIGKSHQGLKLYAVEISDHGEHEVGEPEF
HYIAGAHGNEVLGRELLLLLVQFVCQEYLARNARIHLVEETRIHVLPSSLNPDGYEKAYEGG
SELGGWSLGRWTHDGIDINNNFPDLNTLLWEAEDRQNVPRKVPNHYIAIPEWFSENATVAA
ETRAVIAMEKIPFVLGGNLQGGELVVAYPYDLVRSPWKTQEHTPTPDDHVFRWLAYSYAST
HRLMTDARRRVCHTEDFQKEEGTVNGASWHTVAGSLNDFSYLHTNCFELSIYVGCDKYPHES
QLPEEWENNRESLIVFMEQVHRGIKGLVRDSHGKGIPNAIIISVEGINHDIRTANDGDYWRLL
NPGEYVVTAKAEGFTASTKNCMVGYDMGATRCDFTLSKTNMARIREIMEKFGKQPVSLPARR
LKLRGRKRRQRG

FIGURE 37

CTAAGAGGACAAG**ATG**AGGCCGGCCTCATTCTCCTAGCCCTCTGTTCTCCITGCCAAGCTGCAGGGG
 ATTTGGGGATGTGGGACCTCCAATTCCAGCCCCGGCTTCAGCTCTTCCCAGGTGACTCCAGCTCCAGC
 TTCAAGCTCCAGCTCCAGGTGGGCTCCAGCTCCAGCGCAGCTAGGCAGCGGAGGTTCTGTGCCCAGTTGTT
 TTCCAATTTCACCGGCTCCGGATGACCGTGGACCTGCCAGTGTCTGTTCCCTGCCAGACACCACCTTC
 CGTGGACAGAGTGAACGCTGGAATTACAGCTCATGTTCTTCAGAAGTTGAGAAAGAACCTTCTAA
 GTGAGGGAAATATGTCCTAAATTAGTGTATGAAAAGAAACTGTTAACCTAACTGTCCGAATTGACATCAT
 GGAGAAGGATACCAATTCTTACACTGAACCTGGACTTCGAGCTGATCAAGGTAGAAGTGAAGGAGATGGAAAAAC
 TGGTCATACAGCTGAAGGAGAGTTGGTGGAAAGCTCAGAAATTGTTGACAGCTGGAGGTGGAGATAAGAAAT
 ATGACTCTCTGGTAGAGAAGCTTGAGACACTAGACAAAAAACATGTCCTGCCATTGCCAGAAATCGTGGC
 TCTGAAGACCAAGCTGAAAGAGTGTGAGGCCTCTAAAGATCAAACACCCCTGTCGTCACCTCCACTC
 CAGGGAGCTGTTGTCATGGTGGTGTGGTGAACATCAGCAAAACCGTCTGGTTCACTGTCACCTGGAGAGGTT
 TCTTATCTATATGTTGCTGGGATTACTCTCCCAGCATCAAACAAAGGACTGTATTGGTGGGCC
 ATTGAATACAGATGGGAGACTGTTGGAGTATTATAGACTGTACAACACACTGGATGATTGCTATTGTATATAA
 ATGTCGAGAGTTGGGAGATCACCTATGCCAAGGTAGTGGTACAGCAGTTACAACAAACATGTACGTCAC
 ATGTCACACACCGGGAAATTGCCAGAGTTAACCTGACCAACACGATTGCTGACTCAAACCTCCCTAA
 TGCTGCCCTATAATAACCGCTTTCATATGCTAATGTTGCTTGCAGATATTGACTTTGCTGTTGAGATGAGAATG
 GATTGTTGGTTATTATTCACACTGAAGCCAGCTGGTAACATGGTGATTAGTAAACTCAATGACACCACACT
 CAGGTGCTAACACTGGTATACCAAGCAGTATAAACCATCTGCTCTAACGCCCTCATGGTATGTTGGGTTCT
 GTATGCCACCGTACTATGAAACACCAGAACAGAAGAGATTTTACTATTATGACACAAACACAGGGAAAGAGG
 GCAAACATAGACATTGTAATGATAAGATGCAGGAAAAGTGCAGAGCATAACTATAACCCTTTGACCAAGAAA
 CTTTATGTCATAACGATGGTACCTCTGAATTATGATCTTCTGCTTGCAGAAGCCCCAG**TAA**GCTGTTA
 GGAGTTAGGGTGAAGAGAAAATGTTGAAAAAATAGTCTTCTCCACTTACTTAGATATCTGCAGGGGTGT
 CTAAAAGTGTGTCATTTGCAGCAATGTTAGGTGCATAGTTCTACCACACTAGAGATCTAGGACATTGTCT
 TGATTTGGTGAGTTCTCTGGGAATCATCTGCCTCTCAGGCGCATTTGCAATAAAGTCTGCTAGGGTGGGA
 TTGTCAGAGGTCTAGGGCACTGTGGCCTAGTGAAGCCTACTGTGAGGAGGCTTCACTAGAACGCTTAAATT
 GGAATTAAGGAACCTAAACACTCAGTATGGCGTCTAGGGATTCTTGACAGGAAATATTGCCCAATGACTGC
 CTCATCCATGTAGCACCCTAATTCTCCATGCCAGGAAACCTGGGACTTAGTTAGGTAGATTAAATATCT
 GGAGCTCCTCGAGGGACCAATCTCAACTTTTTTCTCCACTAGCACCTGGAATGATGCTTGTATGTGG
 CAGATAAGTAAATTGGCATGCTTATATTACATCTGTAAGTGTGAGTTTATGGAGAGAGGCCTTT
 ATGCATTAATTGTCATGGCAAATAATCCCAGAAGGATCTGAGATGAGGCACCTGCTTTCTCTC
 ATTGTCCACCTACTAAAGTCAGTAGAATCTCTACCTCATAACTCCCTCCAAAGGCAGCTCAGAACAGATTAG
 AACCAAGACTACTAACCAATTCCACCCCCCACAACCCCTTCACTGCCTACTTTAAAAAAATTAAATAGTTT
 CTATGGAACGTACAGATTAGAAAATTAAATTCTTCTTAATTTCATTATGACTTTATTACATGACTCTA
 AGACTATAAGAAAATCTGATGGCAGTGCACAAAGTGTCTAGCATTATGTTATCTAAAGACCTGGAGCATA
 TGTGCACTTATGAGTGTATGTTGCTGATGTAATTGCTTGCCTTGGTAAGCCTGGAACCTGTAAGAAAAT
 GAAAATTAAATTCTAGGACGAGCTATAGAAAAGCTATTGAGAGTATCTAGTTAATCAGTGCAGTAGT
 TGGAAACCTTGTGGTGTATGTGATGTCCTCTGTGCTTGTGAATGACTTTATCATCTAGTCTTGTCTATT
 TCCTTGTGTTCAAGTCCTAGTCTATAGGATTGGCAGTTAAATGCTTACTCCCCCTTTAAAATAAATGAT
 TAAAATGTGCTTGAaaaaaaaaaaaaaaa

FIGURE 38

MRPGLSFLALLFFLGQAAGDLGDVGPPIPS PGFSSFPGV DSSSFSSSRSGSSSRSLGS
GGSVSQLFSNFTGSVDDRGTCQCSVSLPD TFPVDRVERLEFTAHVLSQKFEKELSKVREYV
QLISVYEKKLLNLTVRIDIMEKDTISYTELDFELIKVEVKEMEKLVIQLKESFGGSSEIVDQ
LEVEIRNMTLLVEKLETLDKNNVLAIRREIVALKTKECEASKDQNTPVVHPPPTPGSCGH
GGVNISKPSVVQLNWRGFSYLYGAWGRDYS PQHPNKGLYWAPLNTDGR LLEYYRLYNTLD
DLLLYINARELRITYGQGSGTAVYNNNMYVNMYNTGNIARVNLTNTIAVTQTL PNAAYNNR
FSYANVAWQDIDFAVDENGLWVIYSTEASTGNMVI SKLNDTTLQVLNTWYT KQYKPSASNAF
MVCGVLYATRTMNTRTEEIFYYYDTNTGKEGKLDIVMHKMQE KVQSINYNPFDQKLYVYNDG
YLLNYDLSVLQKPO

FIGURE 39

GCTCTGAAGACCAAGCTGAAAGAGTGTGAGGCCTCTAAAGATCAAACACCCCTGTCGTCCAC
CCTCCTCCCCTCCAGGGAGCTGTGGTATGGTGGTGGTGAACATCAGCAAACCGTCTGT
GGTCAGCTCAACTGGAGAGGGTTTCTTATCTATGGTCTGGGTAGGGATTACTCTC
CCCAGCATCCAACAAAGGNATGTATTGGGNNGGCCATTGAATAACAGATGGGAGACTGTTG
GAGTATTATAGACTGTACAACCCACTGGATGATTGCTATTGTATATAATGCTCGAGAGTT
GC GGATCACCTATGCCAAGGTAGTGGTACAGCAGTTACAACAACATGTACGTCAACA
TGTACAACACCGGGNATATTGCCAGAGTTAACCTGACC

FIGURE 40

TCTCGCAGATAGTAAATAATCTCGAAAGGCAGAAAGAAGCTGTCTCCATCTGTCTGTAT
 CCGCTGCTCTTGTGACGTTGGAGATGGGGAGCGTCCTGGGCTGTGCTCCATGGCGAGCT
 GGATACCATGTTGTGGAAGTGCCCCGTTTGCTATGCCGATGCTGCTTAGTGGAAAC
 AACTCCACTGTAACTAGATTGATCTATGCACTTTCTTGCTGTGGAGTATGTAGCTTG
 TGTAATGTTGATACCAAGGAATGGAAGAACAACTGAATAAGATTCTGGATTTGTGAGAATG
 AGAAAGGTGTTGTCCTGTAACATTGTTGGCTATAAAGCTGTATATCGTTGTGCTTT
 GGTTGGCTATGTTCTATCTCTCTTTACTAATGATAAAGTGAAGAGTAGCAGTGA
 TCCTAGAGCTGCAGTGACAATGGATTGGTCTTAAATTGCTGCAGCAATTGCAATT
 TTATTGGGGCATCTTCATTCCAGAAGGAACCTTACAACGTGTTGTTATGACATTGCA
 GCAGGTGCCCTTGTTCATCCTCATAACACTAGTCTACTTATTGATTGACATTGCA
 GAATGAATGTTGGGTGAAAAAATGGAAGAACAGGAACTCGAGATGTTGGTATGCAGCCTGT
 TATCAGCTACAGCTCTGAATTATCTGCTGTTAGTTGCTATGTCCTGTTCTTGTCTAC
 TACACTCATCCAGGCCAGTGTTCAGAAAACAAGGCAGTCAGTGTCAACATGCTCCTGT
 CGTTGGTGCCTGTAATGTTACTGCCAAAATCCAAGAACATCACACCAAGATCTGTT
 TGTTACAGTCTTCAGTAATTACAGTCTACACAATGTTGACATGGTCAGCTATGACCAAT
 GAACAGAAACAAATTGCAACCCAAGTCTACTAACGATAATTGGCTACAATACAACAGCAC
 TGTCCCAAAGGAAGGGCAGTCAGTCCAGTGGCATGCTCAAGGAATTAGGACTAATTC
 TCTTTGTTGTTGTTGTTGATTTATTCCAGCATCCGTACTTCAACAAATAGTCAGGTTAATAAA
 CTGACTCTAACAAAGTGTGAATCTACATTAAAGATGGGGAGCTAGAAGTGTGATGGATC
 ACTGGAGGATGGGGACGATGTTACCGAGCTGTAGATAATTGAAAGGGATGGTGTCACTTACA
 GTTATTGCTTCTTCACTCATGCTTTCTGGCTCACTTATATCATGATGACCTTAC
 AACGGTCCAGGTATGAACCTCTCGTGAGATGAAAAGTCAGTGGACAGCTGTGGGTTGAA
 AATCTCTCAGTTGGATTGGCATCGTGCTGTTGACACTCGTGGCACCACTTGTTC
 TTACAAATCGTGTGTTGACTTGAGACTCTAGCATGAAAAGTCCCACCTTGATTATTGC
 TTATTGAAAACAGTATTCCAACTTTGTTAAAGTGTGTTGTTGCTTCCATGTAAC
 TTCTCCAGTGTCTGGCATGAATTAGATTACTGCTTGTCAATTGTTGTTATTCTTACCAA
 GTGCATTGATAATGTAAGTGAATTGACAGAGGAAAGTTATGAAATATGGTGTGAGT
 TAGTAAAAGTGGCCATTATTGGGCTTATTCTCTGCTCTATAAGTTGTAAGGAAATGAAAGAGTAAA
 ACAAATTGTTGACTATTAAAATTATATTAGACCTTAAGCTGTTTAGCAAGCATTAAA
 GCAAATGTATGGCTGCCTTGGAAATATTGATGTGTTGCCTGGCAGGATACTGCAAAGAAC
 ATGGTTTATTAAAATTATAAACAAAGTCACTTAAATGCCAGTTGCTGAAAATCTTATA
 AGGTTTACCCCTGATACGGAATTACACAGGTAGGGAGTGTGTTAGGGACAATAGTGTAGG
 TTATGGATGGAGGTGTCGGTACTAAATTGAAATAACGAGTAATAATCTACTTGGGTAGAGA
 TGGCCTTGCACAAAGTGAACCTGTTGGTTGTTAAACTCATGAAAGTATGGGTTCACT
 GGAAATGTTGAACTCTGAAGGATTAGACAAGGTTGAAAAGGATAATCATGGGTTAGA
 AGGAAGTGTGAAAGTCACCTGAAAGTTAGTTGGGCCAGCACGGTAGCTACCCCTT
 GGTAAATCCCAGCACTTGGGAGCTTAAGTGGTAGATTACTGAGGCCAGGAATTGACACCA
 GCTTGGCACATGGTGAACCTGTTCTATAAAAATACTGGCTTGGCATATGCCTGTGGC
 CAGCACTGAGAGGCTAGTGAAGGATTGCTGAGGCCAGGCCAAAGGTTGCAAGTGAAGCA
 CGTCACTGCACTCTAGCTGGCACAGAGTAAGCCAAAAAAATATATATATTGAAATCAAGG
 AGGCAAAATTGACAGGGAAGGAAGTAACGCAAAACACTAGGCTTGTAGGTACTTAT
 ATAAAATCTAGTCCAGTCTCTCATTTAAAAAAATGAAGACACTGAAATAACAGACTTAAATA
 GCTCAGATAGCTAATTAGGAAATTCAAGTTGGCCAATAATAGCATTCTCTGACATTAA
 AAATAATTCTATTCAAAATACATGCAATTGATTACACCTCATACTGTGATAATTATGT
 GATGTTGATTGCTGGTGTCCAGCATGACCCATAAACAGGTAGAAGAATGATGGAATGTTT
 AGAATAAAACTCCTGCTTATAGTATACTACACAGTTCAAAAGATGTTAAAATGCTTTGTAT
 TTACTGCCATGTAATTGAAATATATAGATTATTGTAACCTTCAACCTGAAAATCAAGCAGT
 ATGAGAGTTAGTTATTGTATGTCAGTAGTGTCAATGAAGCTTAAATCTACAATT
 TCTTCTTAAAATATTATTAAATGTGAATGGAATATAACAATTGCTTAATTCCCCAAC
 TTATTCTGTGTGTTAGACATTGTAATTCCACAAATTGAAATGGCTGTGTTTACCTCTAAATAA
 ATGAATTCAAGGAAAAA

FIGURE 41

MGSVLGLCSMASWI PCLCGSAPCLLCRCCPSGNNSTVTRLIYALFLLVGVCVACVMLI PGME
EQLNKIPGFCENEKGVVPCNILVGYKAVYRLCFGlamfyllsllMIKVKS SDPRAAVHNG
FWFFKFAAAIAIIIGAFFIPEGFTTVWFYVGMAGAFCFILIQLVLLIDFAHSWNESWVEKM
EEGNSRCWYAALLSATALNYLLSLVAIVLFFVYYTHPASCSENKA FISVNMLLCVGASVMSI
LPKIQESQPRSGLLQSSVITVYTMYLTWSAMTNEPETNCNPSLLSIIGYNTTSTVPKEGQSV
QWWHAQGIIGLILFLLCVFYSSIRTSNNSQVNKLTLTSDESTLIEDGGARSDGSLEDGDDVH
RAVDNERDGVTVSYSSFFHMLFLASLYIMMTLTNWSRYEPSREMKSQWTAVWVKISSSWIGI
VLYVWTLVAPLVLTNRDFD

FIGURE 42

GCGAGAAAGAAGCTGTCTCCATCTTGTCTGTATCCCGCTGCTTGTGGAGAT
GGGGAGCGTCCCTGGGCTGTGCTCCATGGCGAGCTGGATACCATGTTGTGGAAAGTGCC
CCGTGTTGCTATGCCGATGCTGCCTAGTGGAAACAANTCCACTGTAACTAGATTGATCTA
TGCACCTTTCTTGCTTGGAGTATGTGTAGCTTGTGAATGTTGATACCAGGAATGGAAG
AACAACTGAATAAGATTCCCTGGATTTGTGAGAATGAGAAAGGTGTTGTCCCTGTAACATT
TTGGTTGGCTATAAGCTGTATATCGTTGTGCTTGGTTGGCTATGTTCTATCTTCTTCT
CTCTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTCACAATGGAT
TTTGGTTCTTAAATTGCTGCAGCAATTGCAATTATTATTGGGGC

FIGURE 43

GTTATTGTGAACTTGTGGAGATGGGAGGTCNTGGGGCTGTGTTCCATGGCGAGCTGGATAC
CANGTTGTGTGGAAGTCCCCGTGTTGNTATGCCGATGCTGTCTAGTGGAAACAANTCC
ACTGTAATTAGATTGATNTATGCACTTTNTTGCTTGGAGTANGTGTAGCTTGTGTAAT
GTTGATACCAGGAATGGAAGAACAACTGAATAAGATTCCCTGGATTTGTGAGAATGAGAAAG
GTGTTGTCCTGTAAACATTTGGTTGGCTATAAAGCTGTATATNGTTGTGCTTGGTTG
GCTANGTTCTATNTTCTTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAG
AGCTGCAGTGCACAATGGATTTGGTTAAATTGCTGCAGCAATTGCAATTATTATTG
GGGC

FIGURE 44

AAGAAGCTGTCTCCATCTTGTCTGTATCCGCTGCTCTTGTGAACGTTNTGGAGATGGGGAGC
GTCCTTGGGTTGTGCTCCATGGCGAGCTGGATACCATGTTGTGTAAGTGCCTCGTGT
TGCTATGCCGATGCTGCTTAGTGGAAACAACACTCCACTGTAACTAGATTGATCTATGCACCT
TTCTTGCTTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAGAACAACT
GAATAAGATTCTGGATTTGTGAGAATGAGAAAGGTGTTGTCCTGTAACATTTGGTTG
GCTATAAAGCTGTATATCGTTGTGCTTGGTTGGCTATGTTCTATCTTCTCTCTTTA
CTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTCACAATGGATTGGTT
CTTTAAATTGCTGCAGCAATTGCAATTATTATTGGGGC

FIGURE 45

GCTGTCCTTAGTGGAAACAANTCCAAC TTGTAAC TTGGATTGATCTATGCAC TTTCC TTG
CTTGTGAGTATGTAGCTTGTAATGTTGTTCCCAGGATTGGANGAACAACTGAATA
AGATTCTGGATTTGTGAGAATGAGAAAGGTGTTGTCCTGTAAACATTTGGTTGGC
TATAAAGCTGTATATCGTTGTGCTTGGCTATGTTCTATCTTCTCTCTTTACT
AATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTCACAATGGATTTGGTCT
TTAAATTGCTGCAGCAATTGCAATTATTATTGGGGCATTCTCATTCCAGAAGGAAC TTT
ACAAC TGTGGTTTATGTAGGCATGGCAGGTGCCTTGTTCATCCTCATACAACTAGT
CTTACTTATTGATTTGCACATTGAAATGAATCGTGGTTGAAAAAATGGAAGAAGGGA
ACTCGAGATGTTGGTATGCAGCCTGTTACAGCTACAGCTCTGAATTATCTGCTGTCTTA
GTTGCTATCGTCCTGTTCTTGTCTACTACACTCATCCAGCCAGTTGTCAGAAAACAAGGC
GTTCATCAGTGTCAACATGCTCCTCTGCGTTGGTGCTCTGTAATG

FIGURE 46

CTCGGGCGCGCACAGGCAGCTCGTTGCCCTCGGATTGAGCTGCGGGTGC CGGGCGCCGGCCTCTCCAAT
 GGCAAATGTGTGGCTGGAGGCAGCGAGGCTTCGGCAAAGGCAGTCAGTGTCAGACCGGGCGAG
 TCCTGTGAAAGCAGATAAAAGAAAACATTATTAACGTGTCATTACGAGGGAGCGCCGGCCGGGCTGTCGC
 ACTCCCCCGGAACATTTGGCTCCCTCCAGCTCCGAGAGAGGAGAAGAAGAAGCGAAAAGAGGCAGATTACAC
 GTCGTTCCAGCCAAGTGGACCTGATCGATGCCCTCCTGAATTACAGATATTGATTATTAGCGATGCC
 CCCTGGTTGTGTTACGCACACACAGTCACACAAGGCTCGGCTCGCTCCCTCCCTCGTTCCAGCTCC
 TGGCGAATCCCACATCTGTTCAACTCTCCGCCGAGGGCGAGCAGGAGCGAGGTGTCGAATCTGCGAGTG
 AAGAGGGACGAGGGAAAAGAACAAAGCCACAGACGCAACTTGAGACTCCGCATCCAAAAGAACGACCAGAT
 CAGAAAAAGAAGATGGGCCCCCGAGCCTCGTGTGCTGCTGCTCCGCAACTGTGTTCTCCTGCTGGG
 TGGAAAGCTCGGCCTCCGTGCGCACCCGCCTGAAAGGCAGGTTTCAGAGGGACCGCAGGAACATCCGCCCA
 ACATCATCCTGGTGTGACGGACGACAGGATGTGGAGCTGGGTTCCATCGAGGTGATGAACAAGACCCGGCG
 ATCATGGAGCAGGGCGGGGCCACTTCATCAACGCCCTCGTGUCCACACCCATGTGTCGCCCTCACGCTCCTC
 CATCCTCACTGGCAAGTACGCCAACACACACACACAACTACACAAATGAGAAGTGTCTCGCCCTCCTGGC
 AGGCACAGCACGAGAGGCCACCTTGGCTGTACCTCAATAGCACTGGTACCGGACAGCTTCTCGGAAG
 TATCTTAATGAATACAAGGCTCCATCGTGTGCCACCCGGCTGGAGGAGTGGGTCGGACTCCTTAAAACCTCCG
 CTTTTATAACTACACGCTGTGCGAACGGGGTGAAGAGAACGACGGCTCCGACTACTCCAAGGATTACCTA
 CAGACCTCATCACCAATGACAGCGTGAGCTTCTCCGCACGTTCAAGAAGATGTACCCGCACAGGCCAGTCCTC
 ATGGTCATCAGCCATGCAGCCCCCACGGCCCTGAGGATTGAGCCCAACATATTCAACGCCCTTCCAAACGC
 ATCTCAGCACATCACGCCAGCTACAACACTACGCCCAACCCGGACAAACACTGGATCATGCGTACACGGGC
 CCATGAAGCCCATCCACATGGATTCAACACATGCTCCAGCGGAAGCGCTTGAGACCCCTCATGCGGGAC
 GACTCCATGGAGACGATTACAACATGCTGGTTGAGACGGGCGAGCTGGACAACACGTACATGTATAACCGC
 CGACCACGGTTACACACATGCCAGTTGGCTGGTGAAGGGAAATCCATGCCATATGAGTTGACATCAGGG
 TCCCGTTCTACGTGAGGGGCCCAACGTTGGAGCAGCCGGCTGTCTGAATCCCCACATGCTCCTCAACATTGACCTG
 GCCCCCCACCATCTGGACATTGAGCCCTGGACATACCTGCGGATATGGACGGGAAATCCATCCTCAAGCTGCT
 GGACACGGAGCGGGCGGTGAATCGGTTCACTTGAAAAAGAAGATGAGGGTCTGGCGGGACTCCTTCTGGTGG
 AGAGAGGCAAGCTGCTACACAAGAGAGACAATGACAAGGTGGACGCCAGGAGGAGAACTTCTGCCAAGTAC
 CAGCGTGTGAAGGACCTGTGTCAGCGTGTGAGTACCAAGACGGCTGTGAGCAGCTGGGACAGAAGTGGCAGTG
 TGTGGAGGAGCCACGGGAAGCTGAAGCTGCATAAGTGAAGGGCCCATGCGGCTGGCGGGAGCAGAGGCC
 TCTCCAACCTGTGCCAAGTACTACGGCAGGGCAGCGAGGCCCTGCACCTGTGACAGCGGGACTACAAGCTC
 AGCCTGGCCGGACGCCGGAAAAACTCTCAAGAAGAAGTACAAGGCCAGCTATGTCGCCAGTCGCTCCATCCG
 CTCAGTGGCATGAGGTGGACGCCAGGGGTGTACACAGTACGGCTGGGTGATGCCGCCAGCCCCGAAACCTCA
 CCAAGCCGCACTGCCAGGGGCCCTGAGGGACCAAGATGACAAGGATGGGGACTTCAGTGGCACTGGAGG
 CTTCGGACTACTCACGCCCAACCCCTATTAAAGTGACACATCGGTGCTACATCTAGAGAACGACACAGTCCA
 GTGTGACCTGGACCTGTACAAGTCCCTGCAGGCCCTGGAAAGACCAAGCTGCACATCGACCGAGATTGAAA
 CCCTGAGAACAAAATTAGAACCTGAGGGAGTCGAGGTGACCTGAAGAAAAGCGGCCAGAACGAGATGTGAC
 TGTCACAAAATCAGCTACCAACCCAGCACAAAGGCCCTCAAGCAGAGGGCTCAGTGTGACATCCTTCAG
 GAAGGGCCTGCAAGAGAACAGGTGTGGCTGTGGAGCAGAAGCGCAAGAACGAGAAACTCCGCAAGCTGC
 TCAAGCGCCTGAGAACACAGACAGTCAGCATGCCAGGCCCTACGTGCTTACCCACGACAACCGACTGG
 CAGACGGCCCTTCTGGACACTGGGCCCTTCTGTGCCCTGCACCGGCCAACAAACACGTACTGGTGCAT
 GAGGACCATCAATGAGACTACAATTCTCTCTGTGAATTGCAACTGGCTCCTAGAGTACTTGATCTCA
 ACACAGACCCCTACCAGCTGATGAATGCACTGGACAGGGATGTGCTCAACCAGCTACACGTACAG
 CTCATGGAGCTGAGGAGCTGCAAGGGTTACAAGCAGTGTAAACCCCGGACTCGAAACATGGACCTGGATGGAGG
 AAGCTATGAGCAATAACAGGCAGTTCACTGGAGCTGAAAGTGGCCAGAAATGAAGAGACCTCTTCAAATCACTGG
 GACAACGTGGGAAGGCTGGGAAGGT**TAA**GAAACACAGAGGTGGACCTCCAAAACATAGAGGCATCACCTGA
 CTGCACAGGAATGAAAACCATGTGGGTGATTCAGCAGACCTGTGCTATTGGCAGGAGGCCGTGAGAACG
 AACGACCGACTCTCAGTCAACATGACAGATTCTGGAGGATAACCAGCAGGAGCAGAGATAACTCAGGAAGTCC
 ATTTTGCCCTGCTTGCTTGATTATACCTCACAGCTGCACAAATGATTTCTGATCAAAGTC
 ACCACTAACCTCCCCAGAAGCTCACAAAGAAAACGGAGAGAGCGAGCGAGAGAGATTCCTGGAAATTTC
 TCCCAAGGGCGAAAGTCATTGGAATTTTAAATCATAGGGAAAAGCAGTCGTTCTAAATCCTCTATTCTT
 TTGGTTGTCAAAAGAAGGAACTAAGAAGCAGGACAGAGGCCACGTGGAGAGGCTGAAAACAGTGCAGAGACG
 TTTGACAATGAGTCAGTAGCAGAACAAAGAGATGACATTACCTAGCACTATAACCCCTGGTGCTCTGAAGAAA
 CTGCCTCATGTATATATGTGACTATTACATGTAATCAACATGGAACTTTAGGGAACCTAATAAGAAAAT
 CCCAATTTCAGGAGTGGTGGTCAATAAACGCTGTGGCAGTGTAAAAGAAAA

FIGURE 47

MGPPSLVLCLLSATVFSLLGGSSAFLSHHRLKGRFQRDRRNIRPNIILVLTDDQDVELGSMQ
VMNKTRRIMEQGGAHFINAFTPMCCPSRSSILTGYVHNHNTYTNNECSSPSWQAQHES
RTFAVYLNSTGYRTAFFGKYLNEYNGSYVPPGWKEVGLLKNSRFYNYTLCRNGVKEKGSD
YSKDYLTDLITNDSVSFRTSKKMYPHRPVLMVISHAAPHGPEDSAPQYSRLFPNASQHITP
SYNYAPNPDKHWIMRYTGPMKPIHMEFTNMLQRKRLQTLMSVDDSMETIYNMLVETGELDNT
YIVYTADHGYHIGQFGLVKGKSMPYEFDIRPFYVRGPNEAGCLNPHIVLNIDLAPTIIDI
AGLDIPADMGDGSILKLLDTERPVNRFHKKMRVWRDSFLVERGKLLHKRDNDKVDAQEEN
FLPKYQRVKDLCQRAEYQTACEQLGQKWQCVEDATGKLKLHKCKGPMRLGGSRALSNLVPKY
YGQGSEACTCDSGDYKLSLAGRRKKLFKKYKASYVRSRSIRSVAIEVDGRVYHVGLGAAQ
PRNLTKRHWPGAPEDQDDKDGGDFSGTGGLPDYSAANPIKVTHRACYILENDTVQCDLDLYKS
LQAWKDHKLHIDHEIETLQNKIKNLREVRGHLKKRPEECDCCHKISYHTQHKGRLKHRGSSL
HPFRKGLQEKDVKWLLREQKRKKLRKLLKRLQNNDTCSMPGLTCFTHDNQHWQTAPFWTLG
PFCACTSANNTYWCMRTINETHNFLCEFATGFLEYFDLNTDPYQLMNAVNTLDRDVLNQL
HVQLMELRSCKGYKQCNPRTRNMDLDGGSYEQYRQFQRRKWEPMKRSSKSLGQLWEGWEG

FIGURE 48

AACAAAGTTCAGTGACTGAGAGGGCTGAGCGGAGGCTGCTGAAGGGGAGAAAGGAGTGAGGA
GCTGCTGGGCAGAGAGGGACTGTCCGGCTCCCAGATGCTGGCCTCCTGGGGAGCACAGCCC
TCGTGGGATGGATCACAGGTGCTGCTGTGGCGGTCTGCTGCTGCTGCTGCTGGCCACC
TGCCTTTCCACGGACGGCAGGACTGTGACGTGGAGAGGAACCGTACAGCTGCAGGGGAAA
CCGAGTCCGCCGGGCCAGCCTGGCCCTTCCGGCGGCCACCTGGGAATTTCA
ATCACCGTCATCCTGGCCACGTATCTCATGTGCCAATGTGGCCTCCACCACCA
CCCCGCCACACCCCTACCACCTCCACCACCACCCCCACCGCCACCATCCCCGCCA
CGCTCGCTGAGGGCTGCTGTCGCCGGTGCCTGTGGACAGCAGCTGCCCTGCCCTCCATCTG
TTCCCAGGACAAGTGGACCCATGTTCCATGTGGAAGGATGCATCTCTGGGTGAACGAGG
GGAACAATAGACTGGGGCTTGCTCCAGCTGCATTGCATGGCATGCCCAAGTGTACTATGGC
AGCAGAGAACATGGAGGAACACTGGGTCTGCAGTGCTGAAGGGTTGGGAGTGGAGAGCAAGG
GTGCTTTGGGGCTGGACAGCCGTCTGTGACAGTGACTCCCAGTGAGCCCCAGAAATG
ACAAGCGTGTCTGGCAGGCCAGCACACAAGTGGATGTGAAGTGCCGTCTGACCTCCTC
ATCAGGCTGCTGCAGGCCTCTGGCGGGCAGGGCACTGGGAGAGGCCCTGAGAATGTCCTTT
GGTTGGAGAAGGCAGTGTGAGGCTGCACAGTCAATTGATCGGTGCCTTAGTCCAAGAAAAT
AAAAACCACTAAGAAGCTTAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 49

MLGLLGSTALVGWITGAAVAVLLLLLLATCLFHGRQDCDVERNRTAAGGNVRRAQPWPFR
RRGHLGIFHHHRHPGHVSHVPNVGLHHHHPRHTPHLHHHHHPRHHPRHAR

FIGURE 50

GGCGGCTGCTGAGCTGCCTTGAGGTGCAGTGGTGGGGATCCAGAGCC**ATG**TCGGACCTGCTA
 CTACTGGGCCTGATTGGGGCCTGACTCTCTTACTGCTGCTGACGCTGCTGGCCTTGCCGG
 GTACTCAGGGCTACTGGCTGGGTGGAAGTGAGTGCTGGTCACCCCCCATCCGCAACGTCA
 CTGTGGCCTACAAGTTCCACATGGGCTCTATGGTGAGACTGGCGGCTTTCACTGAGAGC
 TGCAGCATCTCTCCAAGCTCCGCTCCATCGCTGTACTATGACAACCCCCACATGGTGCC
 CCCTGATAAGTGCCGATGTGCCGTGGCAGCATTGAGTGAAGGTGAGGAATGCCCTCCC
 CTGAGCTCATCGACCTCTACCAGAAATTGGCTCAAGGTGTTCTCCTCCGGCACCCAGC
 CATGTGGTGACAGCCACCTTCCCCTACACCACATTCTGTCCATCTGGCTGGCTACCCGCCG
 TGTCCATCCTGCCTGGACACCTACATCAAGGAGCGGAAGCTGTGTCCTATCCTCGGCTGG
 AGATCTACCAGGAAGACCAGATCCATTTCATGTGCCACTGGCACGGCAGGGAGACTTCTAT
 GTGCCTGAGATGAAGGAGACAGAGTGGAAATGGCGGGGCTTGTGGAGGCCATTGACACCCA
 GGTGGATGGCACAGGAGCTGACACAATGAGTGACACGAGTTCTGTAAGCTTGGAAAGTGAGCC
 CTGGCAGCCGGGAGACTTCAGCTGCCACACTGTCACCTGGCGAGCAGCCGTGGCTGGGAT
 GACGGTGACACCGCAGCGAGCACAGCTACAGCGAGTCAGGTGCCAGCGCTCCTTTGA
 GGAGCTGGACTTGGAGGGCGAGGGCCCTTAGGGAGTCACGGCTGGACCCCTGGGACTGAGC
 CCCTGGGACTACCAAGTGGCTTGGAGCCCCTGAGAAGGGCAAGGAG**TAA**CCC
 ATGGCCTGCACCCCTCTGCAGTGCAGTTGCTGAGGAAGTGAGCAGACTCTCCAGCAGACTCT
 CCAGCCCTTCCCTCTGGGGAGGAGGGGTTCTGAGGGACCTGACTTCCCTGC
 TCCAGGCCTCTGCTAACGCTTCTCCTGAGGCTCCAGGGCAGAGGAGGCC
 GGGACTATTTCTGCACCAGCCCCAGGGCTGCCGCCCCTGTTGTCTTTTCAGACTC
 ACAGTGGAGCTTCCAGGACCCAGAATAAGCCAATGATTACTGTTCACCTGGAAAAAAA
 AAAAAAAA

FIGURE 51

MSDLLLGLIGGLTLLLLTLLAFAGYSGLLAGVEVSAGSPPIRNVTVAYKFMGLYGETGR
LFTESCSISPKLRSIAVYYDNPHMPPDKRCAVGSILSEGEESPSPELIDLYQKFGFKVFS
FPAPSHVVATFPYTTIISIWLATRRVHPALDTYIKERKLCAYPRLEIYQEDQIHFMCPALAR
QGDFYVPEMKETEWKWRGLVEAIDTQVDGTGADTMSDTSSVSLEVSPGSRETSAAATLSPGAS
SRGWDDGDTRSEHSYSESGASGSSFEELDLEGEGPLGESRLDPGTEPLGTTKWLWEPTAPEK
GKE

FIGURE 52

CCGCAGGAACGCTGTCTGGCTGCCGCCACCGAACAGCCTGCTGGTGCCTGGCTCCCT
GCCCGCGCCCAGTCATGACCCCTGCGCCCTCACTCCTCCGCTCCATCTGCTGCTGCT
GCTGCTCAGTGCAGGGCTGAGGCTGGCTCGAAACCGAAAGTCCCGTCCGGA
CCCTCCAAGTGGAGACCCCTGGTGGAGCCCCAGAACCATGTGCCGAGCCCGCTGCTTTGGA
GACACGCTTCACATACACTACACGGGAAGCTGGTAGATGGACGTATTATTGACACCTCCCT
GACCAGAGACCCCTGGTTATAGAACTTGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGA
GTCTTCTCGACATGTGTGGAGAGAACGGAAGGGCAATCATTCTCTCACTTGGCCTAT
GGAAAACGGGGATTCACCCTGTCCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCT
GATTGCACTAATCCGAGCCAACACTGGCTAAAGCTGGTAGAGGGCATTGCGCTCTGGTAG
GGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCACCTATAACAGAAAGGCCAAT
AGACCCAAAGTCTCCAAAAAGAAGCTCAAGGAAGAGAACGAAACAAGAGCAAAAGAAATA
ATAAATAATAAATTTAAAAACTTAAAAAAAAAAAAAA

FIGURE 53

MTLRPSLLPLHLLLLLSSAVCRAEAGLETESPVRTLQVETLVEPPEPCAEPAAFGDTLHI
HYTGSVLVDGRIIDTSLTRDPLVIELGQKQVIPGLEQSLLDMCVGEKRRAIIPSHLAYGKRGF
PPSVPADAVVQYDVELIALIRANYWLKLVKGILPLVGMAMVPALLGLIGYHLYRKANRPKVS
KKKLKEEKRNKSKKK

FIGURE 54

CCCGGGAACGTGTTCTGGCTGCCGCACCGAACAGCCTGTCCTGGTCCCCGGCTCCCTGC
CCCGCGCCCAGTCATGACCCTGCGCCCTCACTCCTCCGCTCCATCTGCTGCTGCTGC
TGCTCAGTGGGGCGGTGTGCCGGCTGAGGCTGGCTCGAAACCGAAAGTCCCGTCCGGACC
CTCCAAGTGGAGACCCTGGTGGAGCCCCCAGAACCATGTGCCGAGCCGCTGCTTTGGAGA
CACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCTGA
CCAGAGACCCTCTGGTTATAGAACTTGGCAAAAGCAGGTGATTCCAGGTCTGGAGCAGAGT
CTTCTCGACATGTGTGGAGAGAACGGAAGGGCAATCATTCCCTCACTTGGCTATGG
AAAACGGGGATTCCACCCTGTCCCAGCGGATGCAGTGGTCAGTATGACGTGGAGCTGA
TTGCACTAATCCGAGCCAACTAAGCTGGCTAAAGCTGGTAGAGGGCATTTCGCCTCTGGTAGGG
ATGGCCATGGTGCCACCCTCCTGGGCTCATTGGGTATCACCTATAACAGAAAGGCCAATAGA
CCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAGAAATAATA
AATAATAAATTTAAAAACTTA

FIGURE 55

CCGAAAGTCCCGTCCGGACCCTCCAAGTGGAGACCCCTGGTGGAGCCCCAGAACCATGTGCC
GAGCCCGCTGCTTGAGACACGCTTCACATACACTACACGGGAAGCTGGTAGATGGACG
TATTATTGACACCTCCCTGACCAGAGACCCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGA
TTCCAGGTCTGGAGCAGAGTCTTCGACATGTGTGGGAGAGAAGCGAAGGGCAATCATT
CCTTCTCACTTGGCCTATGGAAACGGGGATTTCCACCATCTGTCCCAGCGGATGCAGTGGT
GCAGTATGACGTGGAGCTGATTGCACTAATCCGAGCCAACTAAGCTGGCTAAAGCTGGTGAAGG
GCATTTGCCTCTGGTAGGGATGCCATGGTGCAGCCCTCCTGGCCTCATTGGGTATCAC
CTATACAGAAAGGCCAATAGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAA
CAAGAGCAAAAGAAATAATAATAATAATTTAAAAAAACTTAAAA

FIGURE 56

CTGCTGCATCCGGGTCTGGAGGCTGTGCCGTTGTTCTGGCTAAATCGGGGAG
 TGAGGCAGGCCGGCGCGACACCGGGCTCGGAACCACTGCACGACGGGCTGGACTG
 ACCTGAAAAAA**ATG**TCTGGATTCTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGG
 GAAAAGCGCAATACTATTGCTTCATTGCTGCTGGTGTACTATTTTACAGGCTGGTGGAT
 TATCATAGATGCAGCTGTATTATCCCACCATGAAAGATTCAACCACTCATACCATGCCT
 GTGGTGTATAGCAACCAGCCTCTTAATGATTAATGCAGTATCGAATGGACAAGTCCGA
 GGTGATAGTTACAGTGAAGGTTCTGGTCAAACAGGTGCTCGCATTGGCTTCGTTGG
 TTTCATGTTGGCCTTGGATCTGATTGCATCTGTGGATTCTTTGGAGGTTATGTTG
 CTAAAGAAAAAGACATAGTATAACCTGGAATTGCTGTATTTCCAGAATGCCTTCATCTT
 TTTGGAGGGCTGGTTTAAGTTGCCGCAGTAAGACTTATGGCAG**TGA**ACACATCTGAT
 TTCCCACAGCACAAACAGCCCTGCATGGTTGTTTTACTGCTCACTCCAACCTT
 TTGTAATGCCATTTCTAAACTTATTCTGAGTGTAGTCTCAGCTAAAGTTGTGTAATACT
 AAAATCACGAGAACACCTAAACAACACAAAAATCTATTGTGGTATGCACTTGATTAACCT
 ATAAAATGTTAGAGGAAACTTCACATGAATAATTGTCAAATTTATCATGGTATAATT
 TGTAAAAATAAAAGAAATTACAAAAGAAATTATGGATTGTCAATGTAAGTATTGTCATA
 TCTGAGGTCCAAACACAAATGAAAGTGCTCTGAAGATTAAATGTGTTATTCAAATGTGGT
 CTCTCTGTGTCATGAAATGAAATATAACATTAGTTTAAATATTCCGTGG
 TCAAAATTCTCCTCACTATAATTGGTATTACTTTACAAAAATTCTGTGAACATGTAAT
 GTAATGGCTTGAGGGTCTCCAAGGGGTGAGTGGACGTGTTGGAAGAGAGAACCAT
 GGTCCAGGCCACCAGGCTCCCTGTGTCCTCCATGGAAAGGTCTCCGCTGTGCCTCTCATT
 CCAAGGGCAGGAAGATGTGACTCAGCCATGACACGTGGTCTGGTGGATGCACAGTCAC
 CACATCCACCACTG

FIGURE 57

MSGFLEGLRCSECIDWGEKRNTIASIAAGVLFFTGWIIIIDAIVIYPTMKDFNHSYHACGVI
ATIAFLMINAVSNGQVRGDSYSEGCLGQTGARIWLFGFMLAFGSLIASMWILFGGYVAKEK
DIVYPGIAVFFQNAFIFFGGLVFKFGRTEDLWQ

FIGURE 58

TTCTTGGCTAAATCGGGGGAGTGAGGC GGCGCGCGACACCGGGCTCCGGAACC
ACTGCACGACGGGGCTGGACTGACCTGAAAAAAATGTCTGGATTCTAGAGGGCTTGAGATG
CTCAGAATGCATTGACTGGGGGAAAAGCGCAATACTATTGCTTCATTGCTGCTGGTGTAC
TATTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGTTATTATCCCACCATGAAAGAT
TTCAACCACTCATACCATGCCTGTGGTGTATAGCAACCATAGCCTCCTAATGATTAATGC
AGTATCGAACATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTG
CTCGCATTGGCTTTCGTTGGTTCATGTTGGCCTTGGATCTCTGATTGCATCTATGTGG
ATTCTTTGGAGGTTATGTTGCTAAAGAAAAGACATAGTATACCCTGGAATTGCTGTATT
TTTCCAGAACATGCCTTCATCTTTTGAGGGCTGGTTTAAGTTGGC

FIGURE 59

TGGACGGACCTGAAAAAAATGTTGGATTNTAGAGGGNTTGAGATGTTCAGAATGCATGAC
TGGGGAAAAGCGCAAATACTATTGCTTCATTGCTGCTGGTGTANTATTTTACAGGCTG
GTGGATTATCATAGATGCAGNTGTTATTATCCCACCATGAAAGATTCAACCANTCATACC
ATGCCTGTGGTGTATAGCAACCATAGCCTCNTAATGATTAATGCAGTATCGAATGGACAA
GTCCGAGGTGATAGTTACAGTGAAGGTTGGTCAAACAGGTGCTCGCATGGCTTT
CGTTGGTTTCATGTTGGCCTTGGATCTGATTGCATCTATGTGGATTCTTTGGAGGTT
ATGTTGCTAAAGAAAAAGACATAGTATACCCCTGGAATTGNTGTATTTTCCAGAATGCCTTC
ATCTTTTGAGGGCTGGTTTAAGTTGGCCGCACTGAAGANTTATGGCAGTG

FIGURE 60

GGACACCGGGTCCGGACCAATGCANGACGGGTGGANTGACCTGAAAAAAATGTTGGATT
TTTAGAGGGCTTGAGATGNTCAGAATGCATTGACTGGGGAAAAGCGCAATANTATTGCTT
CCATTGCTGCTGGTGTACTATTTTACAGGGTGGATTATCATAGATGCAGCTGTTATT
TATCCCACCATGAAAGATTNAACCACTCATACCATGCCTGTGGTGTATAGCAACCATA
CTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATA
GTGTTGGGTCAAACAGGTGNTCGCATTGGCTTTCGTTGGTTCATGTTGGCCTTGGATT
CTGATTGNATTCTATGCGGATTCTCTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTAT
ACCCTGGAATTNCTNTATTTCCAGAATGCC

FIGURE 61

TAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGAAAAGCGCAATANTATTGCTTCC
ATTGNTGNTGGTGTANTATTTTACAGGCTGGTGGATTATNATAGATGCAGCTGTTATTT
ATCCCACCATGAAAGATTNAACCANTCATACCATGCCTGTGGTGTATAGCAACCATAAGCC
TTCCTAATGATTAATGCAGTATNGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTG
TTTGGGTCAAACAGGTGNTNGCATTGGCTTTNGTGGTTCATGTTGGCCTTGGATCTN
TGATTGCATTTATGTGGATTNTTTGGAGGTTATGTTGCTAAAGNAAAAGACATAGTATAC
CCTGT

FIGURE 62

GGGAGGCTGTGNCCGTTGTTNTTGGCTAAAATCGGGGAGTGAGGC GGCCC GGCGCG
CGNGACACC GGTTCCGGGAACCATTGCACGACGGGTGGACTGACCTGAAAAAAATGTTG
GATTNTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGAAAAGCGCAATACTATT
GCTTCATTGCTGCTGGTGTACTATTTTACAGGCTGGTGGATTATCATAGATGCAGCTGT
TATTTATCCCACCATGAAAGATTCAACCACTCATACCATGCCTGTGGTGTATAGCAACCA
TAGCCTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAA
GGTTGTCTGGGTCAAACAGGTGCTGCATTGGCTTTCGTTGGTTCATGTTGGCCTTGG
ATNTCTGATTGCATCTATGTGGATTCTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAG
TATACCTGGAATTGCTGTATTTCCAGAATGCCTCATNTTTTGGAGGGCTG

FIGURE 63

CGACGGCCGGCGTG **ATG** TGGCTTCCGCTGGT GCT CTC GGT GCT GCT GCTGGCCGTCC
TCTGCAAAGTTACTTGGGACTATTCTCTGGCAGCTCCCCGAATCCTTCTCCGAAGATGTC
AAACGGCCCCCAGGCCCTGGTAACTGACAAGGGAGGCCAGGAAGAAGGTTCTCAAACAAAGC
TTTTCAAGCAACCAAGTGCCGGAGAAGCTGGATGTGGTGGTAATTGGCAGTGGCTTGGGG
GCCTGGCTGCAGCTGCAATTCTAGCTAAAGCTGGCAAGCGAGTCCTGGT GCT GGAACACAT
ACCAAGGCAGGGGCTGCTGTATACCTTGGAAAGAAGATGCCCTGAATTGACACAGGAAT
CCATTACATTGGGCGTATGGAAAGAGGGCAGCATGGCCGTTTATCTGGACAGATCACTG
AAGGGCAGCTGGACTGGCTCCCTGTCCCTCTCCTTTGACATCATGGTACTGGAAAGGGCC
AATGGCCGAAAGGAGTACCCCAGTACAGTGGAGAGAAGCCTACATTCAAGGCTCAAGGA
GAAGTTCCACAGGAGGAAGCTATCATTGACAAGTATAAAAGCTGGTTAAGGTGGTATCCA
GTGGAGCCCCCATCCTGTGGAAATTCTCCCATGGCCGTTGGTCAAGCTCCTCGAC
AGGTGTGGGCTGCTGACTCGTTCTCTCCATTCTCAAGCATCCACCCAGAGCCTGGCTGA
GGTCTCGAGCAGCTGGGGCCTCCTCTGAGCTCAGGCACTACAGCTACATCTCCCCA
CTTACGGTGTCAACCCCAACACAGTCCTTCCATGCACGCCCTGCTGGTCAACCAACTAC
ATGAAAGGAGGCTTTATCCCCGAGGGGGTCCAGTGAATTGCTTCCACACCCTGT
GATTCAAGCGGGCTGGGGCGCTGCTCTCACAAAGGCCACTGTGCAAGAGTGTGGTCTGGACT
CAGCTGGGAAAGCCTGTGGTGTCAAGTGTGAAGAAGGGGATGAGCTGGTGAACATCTATTGC
CCCACATCGTGGTCTCCAACGCAGGACTGTTCAACACCTATGAACACCTACTGCCGGGAACGC
CCGCTGCCTGCCAGGTGTGAAGCAGCAACTGGGACGGTGCAGGCCGGCTTAGGCATGACCT
CTGTTTCTATCGCTCGAGGACCCAAGGAAGACCTGCATCTGCCCTCACCAACTAAT
GTTTACTATGACACGGACATGGACCAAGGGGATGGAGCGTACGCTCCATGCCAGGGAA
GGCTCGGGAAACACATCCCCCTCTCTCGTTCTCCATCAGCCTAACAGATCCGACCTGGG
AGGACCGATTCCCAGGCCGTCCACCATGATCATGCTCATACCCACTGCCCTACGAGTGGTT
GAGGAGTGGCAGCGGGAGCTGAAGGGAAAGCGGGCAGTGACTATGAGACCTCAAAAAC
CTTTGTGGAAGCCTATGTCAGTGGTCTGAAACTGTTCCACAGCTGGAGGGGAAGGTGG
AGAGTGTGACTGCAGGATCCCCACTACCAACCAAGTTCTATCTGGCTGCTCCCCGAGGTG
TGCTACGGGGCTGACCATGACCTGGGCCCTGCACCCCTGTGATGGCTCCTTGAGGGC
CCAGAGCCCCATCCCCAACCTCTATCTGACAGGCCAGGATATCTCACCTGTGGACTGGTC
GGGCCCTGCAAGGTGCCCTGCTGTGCAGCAGGCCATCCTGAAGCGGAACTGTACTCAGAC
CTTAAGAATCTGATTCTAGGATCCGGACAGAAGAAAAAGAAT**ATG** TCCATCAGGGAGG
AGTCAGAGGAATTGCCCCATGGCTGGGCATCTCCCTGACTTACCAATAATGCTTCTG
CATTAGTTCTGCACTATAAACACTCTAATTGGTTCTGATGCCCTGAAGAGAGGCCCTAG
TTTAAATCACAAATTCCGAATCTGGGCAATGGAATCACTGCTTCCAGCTGGGCAGGTGAGA
TCTTACGCCTTTATAACATGCCATCCCTACTAATAGGATATTGACTTGGATAGCTTGATG
TCTCATGACGAGCGCGCTCTGCATCCCTACCCATGCCCTAACCTAGTGTCAAAAGCA
ATATCCATCTGTGGATAGAACCCCTGGCAGTGTGTCAGCTAACCTGGTGGGTTCAAGTC
TGTCTGAGGCTCTGCTCTCATTCATTAGTGCAGCTGCACAGTTCTACACTGTCAAGG
GAAAAGGGAGACTAATGAGGCTTAACCTAAACCTGGGCTGGTTTGTTGCCATTCCATA
GGTTGGAGAGCTAGATCTTTGTGCTGGGTTCACTGGCTCTCAGGGGACAGGAAAT
GCCTGTGCTGCCAGTGTGGTCTGGAGCTTGGGTAACAGCAGGATCCATCAGTTAGTA
GGGTGCATGTCAGATGATCATATCCAATTCTATGGAAAGTCCCGGGTCTGCTTCTTATCA
TCGGGGTGGCAGCTGGTCTCAATGTCAGCAGGCCAGGGACTCAGTACCTGAGGCCATCAATCAAGC
CTTATCCACCAAATACACAGGGAAAGGGTGTGAGCAGGGAAAGGGTGCACATCAGGAGTCAGGGCA
TGGACTGGTAAGATGAATACTTGTGGGCTGAAGCAGGCTGGGTAAGGGAGGGAAAGTCACATCAGAAAAGGA
CACAGCAGGGGACAGTGCAGGGAGGTGTGGGTAAGGGAGGGAAAGTCACATCAGAAAAGGA
AAGCCACGGAATGTGTGAAGGCCAGAAATGGCATTGCAAGTTGAAAAAATGACTTTCAAGTTAGT
TAGACAGGTAGGTGAATGCAAGCTCAAGGTTGAAAAAATGACTTTCAAGTTATGTCTTG
GTATCAGACATACGAAAGGTCTTTGTAGTTGTTAATGTAACATTAAATAATTATTG
ATTCCATTGCTTAAAAAAAAAAAAAA

FIGURE 64

MWLPLVLLLAVLLLAVLCKVYLGLFSGSSPNPFSEDVKRPPAPLVTDEARKKVLKQAFSAN
QVPEKLDVVVIGSGFGGLAAAAILAKAGKRVLVLEQHTKAGGCCHTFGKNGLEFDTGIHYIG
RMEEGSIGRFILDQITEGQLDWAPLSSPDFIMVLEGPNGRKEYPMYSGEKAYIQGLKEKFPQ
EEAIIDKYIKLVVVSSGAPHAILLKFLPLPVVQLLDRCGLTRFSPFLQASTQSLAEVLQQ
LGASSELQAVLSYIFPTYGVTNHSFSMHALLVNHYMKGGFYPRGGSSEIAFHТИPVIQRA
GGAVLTKATVQSVLDSAGKACGVSVKGHELNVNIYCPIVVSAGLFNTYEHLLPGNARCLP
GVKQQLGTVRPGLGMTSVFICLRGTKEDLHLPSTNYYVYDMDQAMERYVSMPREEAAEH
IPLLFFAFPSAKDPTWEDRFPGRSTMIMLIPTAYEWFEWQAEKGKRGSDYETFKNSFVEA
SMSVVLKLFPQLEGKVESVTAGSPLTNQFYLAAPRGACYGADHDLGRLHPCVMASLRAQSPI
PNLYLTGQDIFTCGLVGALQGALLCSSAILKRNLSDLKNLDSRIRAQKKKN

FIGURE 65

GCAGCGCGAGGCGGGTGGCTGAGTCCGTGGCAGAGGCAGAGGCACAGCTCTA
 GGGGTTGGCACCGGCCCGAGAGGAGGAATGCGGGTCCGGATAGGGCTGACGCTGCTGCTGTG
 TCGGGTGTGCTGAGCTTGGCCTCGCGTCCTCGGATGAAGAAGGCAGCCAGGATGAATCCT
 TAGATTCCAAGACTACTTGACATCAGATGAGTCAGTAAAGGACCATACTACTGCAGGCAGA
 GTAGTTGCTGGTCAAATATTCTTGATTAGAAGAACTGAATTAGAATCCTCTATTCAAGA
 AGAGGAAGACAGCCTCAAGAGCCAAGAGGGGGAAAGTGTACAGAAGATATCAGCTTCTAG
 AGTCTCAAATCCAGAAAACAAGGACTATGAAGAGCCAAGAAAGTACGGAAACCAGCTTG
 ACCGCCATTGAAGGCACAGCACATGGGGAGCCCTGCCACTTCCCTTTCTTAGATAA
 GGAGTATGATGAATGTACATCAGATGGGAGGGAAAGATGGCAGACTGTGGTGTGCTACAACCT
 ATGACTACAAAGCAGATGAAAAGTGGGCTTTGTGAAACTGAAGAAGAGGCTGCTAACAGA
 CGGCAGATGCAGGAAGCAGAAATGATGTATCAAACCTGAATGAAAATCCTTAATGGAAGCAA
 TAAGAAAAGCaaaaAGAGAAGCATATCGGTATCTCCAAAAGGCAGCAAGCAGTGAACCATA
 CCAAAGCCCTGGAGAGAGTGTATGCTCTTATTGGTATTACTGCCACAGAATATC
 CAGGCAGCGAGAGAGATGTTGAGAAGCTGACTGAGGAAGGCTCTCCAAGGGACAGACTGC
 TCTGGCTTCTGTATGCCCTGGACTTGGTGTAAATTCAAGTCAGGAAAGGCTCTGTAT
 ATTATACATTGGAGCTCTGGGGCAATCTAACATAGCCCACATGGTTGGTAAGTAGACTT
TAGTGGAAGGCTAACATATTAAACATCAGAAGAATTGTGGTTATAGCGGCCACAACATT
 TCAGCTTCATGATCCAGATTGCTGTATTAAGACCAAATATTCAAGTGAACCTCCTCAA
 ATTCTGTTAATGGATATAACACATGGAATCTACATGTAAATGAAAGTTGGTGGAGTCCACA
 ATTTTCTTAAATGATTAGTTGGCTGATTGCCCTAAAAAGAGAGATCTGATAATGGC
 TCTTTTAAATTTCTGTAGTTCAAAATTGTAATGGCTATAGAAAAACACAT
 GAAATATTACAAATATTGCAACAATGCCCTAAGAATTGTTAAATTGAGTTATT
 GTGCAGAATGACTCCAGAGAGCTCTACTTCTGTTTACTTTCATGATTGGCTGTCTTC
 CCATTTATTCTGGTCATTATTGCTAGTGACACTGTGCCTGCTCCAGTAGTCATTTCC
 CTATTTGCTAATTGTTACTTTCTTGCTAATTGGAAGATTAACTCATTAAATAAA
 ATTATGTCTAACAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAA

FIGURE 66

MRVRIGLTLLLCAVLLSLASASSDEEGSQDESLSKTTLTSDESVKDHTTAGRVVAGQIFLD
SEESELESSIQEEEDSLKSQEGERVTEDISFLESVPNENKDYEERPKKVRKPALTAIEGTAHG
EPCHFPFLFLKEYDECTS DGRDGRLWCATTYDYKADEKWGFCETEEAAKRRQMQEAE
YQTGMKILNGSNKSQKREAYRYLQKAASMNHTKALERVSYALLFGDYLQPNTQAAREMFEK
LTEEGSPKGQTALGFLYASGLGVNSSQAKALVYYTFGALGGNLIAHMVLVSRL

FIGURE 67

CTTCCCAGCCCTGTGCCCAAAGCACCTGGAGCATAGCCTGCAGAACTTCTACTTGCCT
GCCTCCCTGCCTCTGGCC**ATG**GCCTGCCGGTGCCTCAGCTTCCTCTGATGGGACCTCCT
GTCAGTTCCCAGACAGTCCTGGCCCAGCTGGATGCACTGCTGGTCTCCCAGGCCAAGTGG
CTCAACTCTCCTGCACGCTCAGCCCCAGCACGTACCACAGGGACTACGGTGTGCCTGG
TACCAGCAGCGGGCAGGCAGTGCCCTCGATATCTCCTCTACTACCGCTCGGAGGAGGATCA
CCACCGGCCTGCTGACATCCCCGATCGATTCTCGGCAGCCAAGGATGAGGCCACAATGCCT
GTGTCCTCACCATTAGTCCCGTGCAGCCTGAAGACGACGCGGATTACTACTGCTCTGTTGGC
TACGGCTTAGTCCC**TAG**GGGTGGGTGTGAGATGGGTGCCTCCCCTGCCTCCATTCT
GCCCTGACCTGGTCCCTTTAAACTTCTTGAGCCTGCTTCCCTCTGTAAAATGGG
TTAATAATATTCAACATGTCAACAAAC

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FIGURE 68

MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPQVAQLSCTLSPQHVTIRDYGVSWYQQRAG
SAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPQPEDDADYYCSVGYGFSP

FIGURE 69

GCCGCCCGCCCCGAGACCGGGCCGGGGCGCGGGGGATGC GGCCC GGGGC
CGATGACCGCGAGCGCACGCCCGGGCCCTGACCCCGCCGCCGCTGAGCCC
CCCGCCGAGGTCCGGACAGGCCGAG**ATGA**CGCCGAGCCCCCTGTTGCTCCTGCTGCCGC
CGCTGCTGCTGGGGCCTTCCCACCGGCCGCCGAGGCCAAAGATGGCGGAC
AAGGTGGTCCCACGGCAGGTGGCCCGACTGTGCGGCTGCACTGCCCCAGTGG
GGGGGACCCGCCGCGCTGACCATGTGGACCAAGGATGGCCGCACCATCCACAGCGGCTGGA
GCCGCTTCCGCGTGTGCCGCAGGGCTGAAGGTGAAGCAGGTGGAGCGGGAGATGCCGC
GTGTACGTGTGCAAGGCCACCAACGGCTTCGGCAGCCTGAGCGTCAACTACACCCCTCGTCGT
GCTGGATGACATTAGCCCAGGAGAGCCTGGGGCCGACAGCTCTGGGGTCAAG
AGGACCCGCCAGCAGCAGTGGCACGCCGCGCTTACACAGCCCTCCAAGATGAGGCCG
CGGGTAGTCGACGCCGGCTGGTAGCTCCGTGCGCTCAAGTGCCTGGCCAGCGGGCACCC
TCGGCCCGACATCACGTGGATGAAGGACGACCAGGCCTGACGCGCCAGAGGCCGCTGAGC
CCAGGAAGAAGAAGTGGACACTGAGCCTGAAGAACCTGCGGCCGGAGGACAGCGGCAAATAC
ACCTGCCGCGTGTGCAACCGCGGGGCCATCAAGGCCACCTACAAGGTGGATGTGATCCA
GCGGACCCGTTCAAGCCCCTGCTCACAGGCACGCACCCCGTAACACGACGGTGGACTTCG
GGGGGACACGTCCCTCACTGCAAGGTGCGCAGCGACGTGAAGCCGGTATCCAGTGGCTG
AAGCGCTGGAGTACGGGCCAGGGCCACAACCTCCACCATCGATGTGGCGGCCAGAA
GTTTGTGGTGCTGCCACGGGTGACGTGTGGTCGCGGCCGACGGCTCCTACCTCAATAAGC
TGCTCATCACCGTGCCGCCAGGACGATGCGGGCATGTACATCTGCCCTGGCGCCAAACACC
ATGGGCTACAGCTCCGCAAGCCTTCAGCGCCTCCCTCACCGTGCTGCCAGACCCAAAACGCCAGGGC
ACCTGTGGCCTCTCGTCCCTGGCCACTAGCCTGCCGTGGCCGTGTCATGGCATCCAG
CCGGCGCTGTCCTCATCTGGGCCACCCCTGCTCTGGCTTGGCAGGGCCAGAAGAAGCCG
TGCACCCCGGCCCTGCCCTCCCTGGCTGGGCCAGCGCCGCCGGGACGGCCGACCG
CAGCGAGACAAGGACCTCCCTGTTGGCCGCCCTCAGCGCTGGCCCTGGTGTGGGCTGT
GTGAGGAGGACATGGGTCTCCGGCAGCCCCCAGCACTACTGGGCCAGGCCAGTTGCTGG
CCTAAGTTGTAACCCAACTCTACAGACATCCACACACACACACACACTCTCACAC
ACACTCACACGTGGAGGGCAAGGTCCACCGCACATCCACTATCAGTGC**TAGACGGCACCGT**
ATCTGAGTGGCACGGGGGGCGGCCAGACAGGCAGACTGGGAGGATGGAGGACGGAGCT
GCAGACGAAGGCAGGGACCCATGGCGAGGAGGAATGGCCAGCACCCAGGCAGTGTG
TGAGGCATAGCCCTGGACACACACAGACACACACTACCTGGATGCATGTATGCAC
ACACATGCGCACACGTGCTCCCTGAAGGCACACGTACGCACACGCACATGCACAGATATG
CCGCTGGCACACAGATAAGCTGCCAAATGCACGCACACGCACAGAGACATGCCAGAAC
TACAAGGACATGCTGCCCTGAACATACACACAGCACCCATGCGCAGATGTGCTGCCCTGGAC
CACACACACACGGATATGCTGCTGGACGCACACAGTCGAGATATGGTATCCGGACACA
CACGTGCACAGATAATGCTGCCCTGGACACACAGATAATGCTGCCCTGGACACACACATGCA
ATATTGCCCTGGACACACACACACACACACACAGATAATGCTGCCCTGGACACACAC
ACATGAGATATGCTGCCCTGGACACACACTTCCAGACACACAGTGCACAGGCAGATAATGCT
GCCTGGACACACGCAGATAATGCTGCTAGTCACACACACAGCAGACATGCTGCCGGACAC
ACACACGCATGCACAGATAATGCTGCCGGACACACACAGCAGCAGATAATGCTGCCCTGGAC
ACACACACAGATAATGCTGCCCTAACACTCACACAGTCGAGATAATTGCCCTGGACACACACA
TGTGCACAGATAATGCTGCTGGACATGCACACACAGTGCAGATAATGCTGCTGCCGGACACACAG
CACGCACACATGCAGATAATGCTGCCCTGGACACACAGATAATGCTGCCCTAACACTCACACAGTC
GCAGATAATGCTGCCCTGGACACACACAGATAATGCTGCCCTAACACTCACACACAGTC
TATTGCCCTGGACACACACATGTGCACAGATAATGCTGCTGGACATGCACACACAGTC
TGCTGCCGGATAACACACGCACGCACACATGCAGATAATGCTGCCCTGGACACACACTTCCGG
CACACATGCACACACAGGTGCAGATAATGCTGCCCTGGACACACAGCAGACTGACGTG
GAGGGTGTGCCGTGAAGCCTGCAGTACAGTGTGCCGTGAGGGCTCATAGTTGATGAGGGACTT
CCCTGCTCCACCGTACTCCCCAAACTCTGCCCTCTGCCCTGCCCTGAGGGCT
CATCCCCGCCCTGTCCCCCTGGCCTGGCGCTATTGGCCACCTGCCCTGGGTGCCAGG
AGTCCCCCTACTGCTGCTGGCTGGGGTGGGGCACAGCAGCCCCAAGCCTGAGAGGGCTGGAG
CCCATGGCTAGTGGCTCATCCCCAGTGCATTCTCCCCCTGACACAGAGAAGGGGCC
TTTATATTAAAGAAATGAAGATAATTAATAATGATGGAAGGAAGACTGGGTTGCAGGGAC
TGTGGTCTCTCTGGGGCCGGACCCGCCCTGGCTTTCAGCCATGCTGATGACCACACCC
GTCCAGGCCAGACACCACCCCCACCCACTGCTGTGGTGGCCAGATCTCTGTAATT
TGTAGAGTTGAGCTGAAGCCCCGTATATTAAACACAAAAA

FIGURE 70

MTPSPLLLLLPPLLLGAFPPAAAARGPPKMADKVVPRQVARLGRTVRLQCPVEGDPPPLTM
WTKDGRTIHSGWSRFRVLPOGLKVKQVEREDAGVYVCKATNGFGSLSVNYTLVVLDDISPGK
ESLGPDSSSGQEDPASQQWARPRFTQPSKMRRIARPVGSSVRLKCVASGHPRPDITWMK
DDQALTRPEAAEPRKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQRTRSKPVL
TGTHPVNTTVDFGGTTSFQCKVRSDVKPVIQWLKRVEYGAEGRHNSTIDVGGQKFVVLPTGD
VWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLTVLPDPKPPGPPVASSSSA
TSLPWPVVIGIPAGAVFILGTLLLWLCQAQKKPCTPAPAPPLPGHRPPGTARDRSGDKDLPS
LAALSAGPGVGLCEEHGSPAAPQHLLGPGPVAGPKLYPKLYTDIHTHTHSHTHVEGKV
HQHIHYQC

FIGURE 71

CCCAGCTGAGGAGCCCTGCTCAAGACACGGTCACTGGATCTGAGAAACTTCCAGGGACCACGCATTCCAGAGTC
 AGTGAACCTGTGAAGCACCCACATCTACCTCTGCCACGTTCCACGGGCTTGGGGAAAGA**ATGGTGGGGACCA**
 AGGCCTGGTGTCTCCTTCTGGTCTGGAGAAGACAGCATCTTGCAAGCCTGCCACACCCTGGAGAGGCCCTGG
 GTAAAGAAGAGTCCAGCCTGGAGAAGAACCCAGCATCTTGCAAGCCTGCCACACCCTGGAGAGGCCCTGG
 TGAGTGGACAACATGGTCAACATCGACTACCCAGCGGGAGGGCAGACTATGAGCGGCTGGACGCCATTGCT
 TCTACTATGGGACCGTGTATGTGCCCGTCCCTGCGGCTAGAGGCTCGGACCACTGACTGGACACCTGGGGC
 AGCACTGCCAGGTGGTCCATGGTAGCTCCCGTGGGGTTCTGGCTCAACAGGGAGCAGCGGCCCTGGCCA
 GAACCTGCTCTAATTACACCGTACGCTCTCTGCCACCGAGATCCCTGCCCGAGACACAGAGCGCATCTGGA
 GCCCATGGTCTCCCTGGAGCAAGTGTCAAGCTGCCGTGGTAGACTGGGCTCAGACTCGCACACGCATTG
 TTGGCAGAGATGGTGTGCGCTGTGCACTGAGGCCAGCGAAGAGGGTCAAGACTGCCATGGGCCAGGACTGTACAGC
 CTGTGACTGTGACTGCCAATGGGCCAGGTGAATGCTGACTGTGACTGCCATGTGCCAGGACTTCATGCTTC
 ATGGGGCTGTCTCCTTGGGGAGGGCTGCCATGGCTCAGGGCTGCTATCTACCTCTGCCATGACCAAGACGCCAG
 CTGCTGCCAGACAGCATGGTAGGGAGATTCCGAATCCCTGGCTGATGGCAAAGACATCTGAA
 GATCACAAAGGTCAAGTTGCCCATTTGTACTCACATGCCAAGACTAGCCTGAAGGCAGCCACCATCAAGG
 CAGAGTTGTGAGGGCAGAGACTCCATACATGGTAGACGCCAGACAAAAGCAGCGAGAGCTGGGCCAGAGC
 GTGCTCTGTGCTGTAAAGGCCACGGGAAGGCCAGGCCAGACAGTATTGGTATCATAAATGACACATTGCT
 GGATCCTCTCCCTCAACAGCATGAGAGCAAGCTGGTGTGAGGAAACTGCAGCAGCACCCAGGCTGGGGAGTACT
 TTTGCAAGGCCAGAGTGTGATGCTGGGGCTGTGAAGTCCAAGGGTGGCCAGCTGATTGTCACAGCATCTGATGAG
 ACTCCTTGCAACCCAGTCTCTGAGAGCTATCTTATCCGGCTGCCCATGATTGCTTCAAGAATGCCACCAACT
 CTTCTACTATGACGTGGACGCTGGCTGTAAAGACTGTGCAAGGGCAGCAGGATAATGGGATCAGGTGCCGTG
 ATGCTGCAAGACTGCTGTGCACTCTCAACAGAGGAAAGGGAGATCAGTGCAGTGGCTACAGCTACCC
 ACCAAGGGGCCAGGAGTGCAGCTGCCAGCGGTGTACGGAAACTCGGAGCATGTCGGGGCCGTGTCACTG
 TGCTGACAATGGGGAGCCCATGCGCTTGGCATGTGTACATGGGAACAGCGCTGTGAAGCATGACTGGCTACA
 AGGGGACCTTCACCCCTCATGCCCCAGGACACTGAGAGGGCTGTGCTCACATTGGACAGGCTGCAAG
 TTTGTCACACCAACCAAAAGTGTACCTTCAACAAAGAAGGGGAGTGGCTGTCCATGAAATCAAGATGCTTC
 TCGGAAAGAGCCATCACTTGAAGCCATGGAGACCAACATCATCCCCCTGGGGAAAGTGGTGGTGAAGACC
 CCATGGCTGAACGGAGATTCCATCCAGGAGTTCTACAGGAGCAATGGGAGCCCTACATAGGAAAAGTGAAG
 GCCAGTGTGACCTTCTGGATCCCGGAAATATTCACACGCCACAGCTGGCCAGACTGACCTGAACCTCATCAA
 TGACGAAGGAGACACTTCCCCCTGGAGCTGTGCTCACAGGCCCCAGGAGCTGAGGAGTCACCTCAG
 AGCCACTTAATGCTGGCAAAGTGAAGGTTCACCTTGACTCGACCCAGGTCAAGATGCCAGAGCACATATCACA
 GTGAAACTCTGGTCACTCAATCCAGACACAGGGCTGTGGGAGGGAGAAGGTGATTCAAATTTGAAAATCAAAG
 GAGGAACAAAAGAGAAGACAGAACCTCTGGTGGCAACCTGGAGATTGAGGAGGAGGCTCTTAACTGG
 ATGTTCTGAAAGCAGGCGTGTCTGGTAAAGGTGAGGGCTACCGGAGTGTGAGAGGGTCTGCTAGTGAGCAG
 ATCCAGGGGGTGTGATCTCCGTGATTAACCTGGAGCCTAGAACTGGCTCTTGTCAACCCCTAGGGCTGGGG
 CGCTTGCAGTGTGATCACAGGCCCCAACAGGGGGCTGTGTGCTGCCCTCTGTGATGACCGAGTCCCCTGATG
 CCTACTGCCTATGTCTGGCAACGCCATGGCTGGGAGGAACTGCAAGCAGTGGAGCTTCTCTAAATTCAAC
 CCAAATGCAATTGGCTCCCTCAGGCTCATCTCAACAGCTCAACTACCGTCGGACGCCATGAGGATCCACG
 GGTAAAAAGAGCAGCTTCCAGATTGAGCTGGCAAGCCAAGGCCAACCTCAGCTGAGGAGAGCAATGGGCCA
 TCTATGCCTTGTGAGAACCTCGGGCATGTGAAGAGGCAACCCCCAGTGCAGGCCACTTCCGGTCTACCA
 GAGGGGGATGCGATGACTAACACAGCAGCTGGCTCTCAACGAAGATGACCCATGAGACTGGAGCTGAAGACTATCT
 GGCATGGGCAAGGCCAGTGGATTCAAGGGCTGTCTATATCAAGGTGAAGATTGTGGGGCACTGGAAGTGA
 ATGTCGATCCCGCAACATGGGGGCACTCATCGGCGGACAGTGGGAAGCTGTATGGAATCCGAGATGTGAGG
 AGCACTCGGGACAGGGACCAGCCAATGTCAGTCAGCTGCCGTCTGGAGTCAAGTGCAGTGGATGCTCATG
 TCAGGGACGTGTGGACGCCACCTGGTAAGGGTACCCCCAGGGCAGCTGCCGTGAGGCCAGTGTGAACCCCA
 TGCTGATGAGTACCTGGTCAACCCTGGCAACTTGCAGTCAACACAGCACCCAGTGTGAGTACACCATGCTGG
 CCCTGGACCCACTGGGCCACAAACTATGGCATCTACACTGTCAGTGCACAGGACCCCTGCACGCCAAGGAGAT
 CGCGCTCGGGCGGTGTTGATGGCACATCGGATGGCTCTCAGAATCATGAAGAGCAATGTGGAGTAGGCC
 TCACCTCAACTGTGTAGAGAGGGCAAGTAGGCCAGAGTGGCTCTCCAGTACCTCCAAAGCACCCAGGCCAG
 TCCCCTGCTGAGGCAACTGTGAGGAGGCTCTGGTCAACAGGCCCTGATCAAC**TAA**TTTTGGGT
 CCAGGGTGGAGTGGTGGCTCTGTGAGATTCTCTAGAGTGTGCTCAACAGGCCCTGATCAAC**TAA**TTTTGGGT
 ACTTCACCCCTTCTGCCCTATTCATGTGACAGCCATTGTGAGACTGATGCAACAAACTGTCACTTGGTTAAT
 TTAAGCACTTCTGTTTCGTGAATTGCTGTTGTTCTCATGCTTACTTACTTGTCTTACTGCTTACTGACTGA
 TTGGCACGGTGGCCCCAACATGGCACAAATAGGCCATTGTAAGAACTGTTCTTAAATGAAACACAAGAAATT
 GGCCACTGGTAAACTCTGCAGCTCAACTGTACTTCATTTAATGCCATTATGCAAAATATACTTCTCTCTT
 TTGCTGATGGTTTGGCCACCTCTGCAATAGTGTGATGATGCTGAAGATCAAATACCAATATAAAAGCATAT
 TTCTTGCCCTGCTCCACAGGACATAGGCAAGCCTGATCATAGTTCTCATACATATAATGGTGGTGAAGATAAAG
 AAATAAAACACAATTTACTTGTGAAATGTAATAACTTATTTCTTGTCAATTGAAATTCTAGTGC
 ACATTCAAAAGTAAAGCTATTAAATATAGGGTGTACAGTGTCTACCAAGTCTGGAAAGAACATCTCCTGGT
 ATCCACAATTACACCAGGTGCTAACTGTATTGTCACATTCCCTTGCATTGCTTTGTTCTGCTAGAAC
 CCAGTGTAGGCCAGGGCAGATGTCAATAATGCATACTCTGTTGAA

FIGURE 72

MVGTKAWVFSFLVLEVTSQLRQMLTQS VRRVQPGKKNPSI FAKP ADTLES PGEWTWFNI
DYPGGKGDYERLDAIRFY YGDRV CARPLR LEARTTDWT PAGSTGQVVHGS PREGFWCLNREQ
RPGQNCNSNYTVRFLCPPGSLRRDTERIWS PWSPWSKCSAACGQTGVQTRTRICLAEMVSLCS
EASEEGQHCMGQDCTACDLTC PMGQVNADCDACMCQDFMLHGA VSLPGGAPASGAAIYL LTK
TPKLLTQTDSDGRFRIPGLCPDGKSILKITKVKFAPIVLTMPKTS LKAATIKA EFVRAETPY
MVMNPETKARRAGQSVSLCCKATGKPRPDKYFWYHNDTLLDPSLYKHE SKLVLRLQQHQAG
EYFCKAQSDAGAVKSKVAQLIVTASDETPCNPVPESYLI RLPHDCFQNATNSFYYDVGRCPV
KTCAGQQDNGIRCRDAVQNCCGISKTEEREIQC SGYTLPTKVAKECSCQRCTETRSIVRGRV
SAADNGEPMRFGHV YMGN SRVSM TGYKGTFTLHVPQ DTERLVLT FVDRLQKFVN TTKVLP FN
KKGS AVFHEIKMLRRKEPI TLEAMETNIIPLGEVVGEDPMAELEIPSRSF YRQN GEPYIGKV
KASVTFLDPRNISTATAAQ TDLNFINDEGDTFPLRTYGMFSVDFRDEV TSEPLNAGKVKVHL
DSTQVKMPEHISTVKLWSLN PDTGLWEEGDFKFENQRRN KREDRTFLVGNLEIRERRLFNL
DVPESRRCFVKVRAYR SERFLPSEQIQGVVI SVINLEPRTGFLSNPRAWGRFD SVITGPNGA
CVPAFCDDQSPDAY SAYVLA SLAGEELQAVESSPKFNPNAIGVPQPYLNKL NYRR TDHEDPR
VKKTAFQISMAKPRPNSAEE SNGPIYAFENLRACEAPP SAAHFRFYQIEGDRYDYNTVPFN
EDDPMSWTEDYLAWWPKPM EFRACYIKVKIVGPLEVNVR SRNMGGTH RRTVGKLYGIRDVRS
TRDRDQPNVSAACLEFKCSGMLYDQDRVDRTLKVVIPQGSCRRASVN PMLHEYLVNHLPLAV
NNDTSEYTM LAPLDPLGHNYGIYTVDQDPRTAKEIALGRCFDGTSDGSSRIMKS NVGVALT
FNCVERQVGRQSAFQYLQSTPAQSPAAGTVQGRVPSRRQQRASRGGQRQGGVVASLRFPRVA
QQPLIN

FIGURE 73

CTGCAAGTTGTTAACGCCTAACACACAAAGTAGTTAGGCTTCCACCAAAGTCCTCAATATACCTGAATAACGCAC
 AATATCTTAACCTTCATATTGGTTTGGGATCTGCTTGAGGTCCCCTTCATTTAAAAAAAATACAGAG
 ACCTACCTACCCGTACGCATAACATACATATGTGTATATATGTAAACTAGACAAAGATCGCAGATCATAAAGC
 AAGCTCTGCTTAGTTCCAAGAAGATTACAAGAATTAGAG**ATGT**ATTGTCAAGATCCCTGTCGATTCATG
 CCCTTGGGTTACGGTGTCTCAGTGATGCAGCCCTACCCTTGGTTGGGGACATTATGATTGTGAAGACT
 CAGATTTACCGGAAGAAGGGAAAGTTGGGATTACATGGCCTGCCAGCCGAATCCACGGACATGACAAAATA
 TCTGAAAGTGAACACTCGATCTCCGGATATTACCTGTGGAGACCTCCTGGAGACGTTCTGTGCAATGGCAATC
 CCTACATGTGCAATAATGAGTGTGATGCGAGTACCCCTGAGCTGGCACACCCCCCTGAGCTGATGTTGATTT
 GAAGGAAGACATCCCTCCACATTGGCAGTCTGCACTTGAAGGAGTATCCCAAGCCTCTCCAGGTTAACAT
 CACTCTGTCTGGAGCAAACATTGAGCTAACAGAACATAGTTTACCTTGAATCTGGCGTCCAGACC
 AAATGATCCTGGAGAAGTCTCTGATTATGGACAAACATGGCAGCCCTATCAGTTTACGCCACAGACTGCTTA
 GATGCTTTACATGGATCCTAAATCCGTGAAGGATTATCACAGCATACTGGCTTAGAAATCATTGACAGA
 AGAGTACTCAACAGGTATAACACAAATAGCAAATAATCCACTTGAATCAAAGACAGGTTCGCGTTTG
 CTGGACCTCGCCTACGCAATATGGCTCCCTACGGACAGCTGGATACAACCAAGAAACTCAGAGATTCTT
 ACAGTCACAGACCTGAGGATAAGGCTGTTAAGACCAGCGTTGGGAAATATTGTAGATGAGCTACACTTGGC
 ACGCTACTTTACCGATCTCAGACATAAGGTGCGAGGAAGGTGCAAGTGTAAATCTCCATGCCACTGTATGT
 TGTTATGACAACAGCAAATTGACATGCGAATGTGAGCACAACACTACAGGCCAGACTGTGGGAAATGCAAGA
 ATTATCAGGCCGACCTGGAGTCCAGGCTCCTATCTCCCCATCCCCAAAGGCACTGCAAATACCTGTATCCC
 CAGTATTCCAGTATTGGTACGAATGTCTGCGACAACGAGCTCTGCACTGCCAGAACGGAGGGACGTGCCACA
 ACAACGTGCGCTGCCGTGCCGGCGCATACACGGGCATCCTCTGCGAGAAGCTGCCGTGCGAGGAGGCTGGC
 AGCTGCCGCTCGACTCTGCCAGGGCGCCCGCACGGCACCCCCAGCGCTGCTGCTGACCACGCTGCT
 GGGAACCGCCAGCCCCCTGGTGTTC**TAG**GTGTCACCTCCAGGCCACACGGACGGCCGTGCCGTGGGAAAGCA
 GACACAACCCAAACATTGCTACTAACATAGGAAACACACACATACAGACACCCCCACTCAGACAGTGTACAAA
 CTAAGAAGGCCTAACTGAACTAACCCATATTATCACCCGTGGACAGCACATCCGAGTCAGACTGTTAATT
 TGACTCCAGAGGAGTTGGCAGTGTGATATTACTGCAAATCACATTGCCAGCTGAGGACATATTGTTG
 TTGGAAAGGCTGCGACAGCCCCAAACAGGAAAGACAAAAACAAACAAATCAACCGACCTAAAAACATTGGC
 TACTCTAGCGTGGTGCCTAGTACGACTCCGCCAGTGTGGACCAACAAATAGCATTCTTGCTGT
 GTGCATTGTGGCATAAGGAAATCTGTTACAAGCTGCCATATTGGCTGCCCTGAATCCCTTCAAC
 CTGTGTTAGTGAACGTTGCTCTGTAACCCCTGTTGGTGAAGATTCTTGTGATGTTAGTGTAC
 TGTGTAACAGCCCCCTCTAAAGCGAACGCCAGTCATACCCCTGTTAGTCTTGTGTTAGCAGCACTGAGTCCAGTGC
 GCACACACCCACTATACAAGAGTGGCTATAGGAAAAAGAAAGTGTATCTATCCTTGTATTCAAATGAAGTT
 ATTTTCTGAACTACTGTAATATGTAGATTGGTATTATGCAATTGCTTGTGTTAGCAGACAATCTGTTAAT
 GTATCTAATTGCAATCAGCAAAGACTGACATTGTTATTTGTCTCTTGTGTTGTTGTTACTGTGAGA
 GATTCTCTGTAAGGGCAACGAACGTGCTGGCATCAAAGAATATCAGTTACATATATAACAAGTGAATAAGA
 TTCCACCAAGGACATTCTAAATGTTCTGTTGCTTAACACTGGAAGATTAAAGAATAAAACTCCTGCA
 TAAACGATTTCAGGAATTGTTGACTGAGTACATTGCAATTCTTAAGATGAAAGGACAGCCACCAAGCAGTT
 CACTTTACTGTTCTGTTGACTGAGTACATTGCAATTGCAATTGTTGACTGAGTACATTGCAATTGTT
 AGCTTGGACAACCTCTGCAAATATGAGACTATTCCACTTGGGAAAATTACAACAGCAAAAAAAA
 AAAAAAA

FIGURE 74

MYLSRSLSIHALWTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMACQPESTDMTKYLK
VKLDPPDITCGDPPETFCAMGNPYMCNNEDASTPELAHPPPELMFDFEGRHPSTFWQSATWK
EYPKPLQVNITLWSKTIELTDNIVTFESGRPDQMILEKSLDYGRTWQPYQYYATDCLDAF
HMDPKSVKDLSQHTVLEIICTEEYSTGYTTNSKIIHFEIKDRFALFAGPRLRNMASLYGQLD
TTKKLRDFFTVDLRIRLLRPAVGEIFVDELHLARYFYAISDIKVRGRCKCNLHATVCVYDN
SKLTCECEHNTTGPDCGKCKNYQGRPSPGSYLPPIPKGTANTCIPSISIGTNVCDNELLH
CQNGGTCHNNVRCLCPAAYTGILCEKLREEAGSCGSDSGQGAPPHTPALLLTTLLGTAS
PLVF

FIGURE 75

CCCACCGCGTCCGGGTGACCTGGGCCGAGCCCTCCCGGCTGGCTAAGATTGCTGAGGAGGC
 CGGGTAGCTGGCAGGCGCCGACTTCCGAAGGCCGCGTCCGGCGAGGTGTCCTCATGACTT
 CTCTTGACCAT**TG**TCCGTGATCTTTTGCTGCGTGGTACGGTAAGGGATGGACTGCC
 CCTCTCAGCCTCTACTGATTTTACACACCCAAGATTTTGAATGGAGGAGACGGCTCA
 AGAGTTAGCCTTGCGACTGGCCCAGTATCCAGGTCGAGGTTCTGCAGAAGGTTGTGACTTT
 AGTATACTTTCTTCTTCGGGGACGTGGCCTGCATGGCTATCTGCTCCTGCCAGTGTCC
 AGCAGCCATGGCCTCTGCTCCTGGAGACCCCTGTGGTGGATTACAGCTTCCTATGACA
 CTACCTGCATTGGCCTAGCCTCCAGGCCATACGCTTTCTTGAGTTGACAGCATCATTAG
 AAAGTGAAGTGGCATTAACTATGTAAGTTCTCTCAGATGGAGTGCAGCTGGAAAAAAAT
 TCAGGAGGAGCTCAAGTTGCAGCCTCCAGCGTTCTCACTCTGGAGGACACAGATGTGGCAA
 ATGGGGTGTGAATGGTCACACACCGATGCACCTGGAGCCTGCTCCTAATTCCGAATGGAA
 CCAGTGACAGCCCTGGGTATCCTCTCCCTATTCTCAACATCATGTGTGCTGCCCTGAATCT
 CATTGAGGAGTTCACCTGCAGAACATTCTTACAGGATCCAAGGAGCTGGTTCTGCTGGT
 TGGACCAAACCTCG**TGA**GCCAGCCACCCCTGACCCAAATGAGGAGAGCTCTGATTCTCCCAT
 CCGGGAGCAGTGATGTCAAACCTCTGCTGCTGGGAAATCTCATCAGCAGGGAGCCTGTGGA
 AAAGGGCATGTCAGTGAAATCTGGAATGGCTGGATTCGAAACATCTGCCATGTGTATTG
 ATGGCAGAGCTGTTGCCACAAGCGCCTTTATTTAGGGTAAAATTAAACAAATCCATTCTAT
 TCCTCTGACCCATGCTTAGTACATATGACCTTAACCCTACATTATGATTCTGGGTT
 GCTTCAGAAGTGTATTTCATGAATCATTATGATTGATCCCCCAGGATTCTATTGTTG
 TTAATGGGCTTTCTACTAAAGCATAAAACTGAGGCTGATTTAGTCAGGGCAAAACCAT
 TTACTTACATATCGTTCAAAACTTGCTGTTCATGTTACACAAGCTTACGGTTTC
 TTGTAACAATAAAATTTGAGTAAATAATGGGTACATTTAACAAACTCAGTAGTACAACC
 TAAACTTGTATAAAAGTGTGTAAAATGTATAGCCATTATCCTATGTATAAATTAAATG
 AGGTGGCTTCAGAAATGGCAGAATAAATCTAAAGTGTATTAAAAAAA
 AAAAG

FIGURE 76

MSV1FFACVVVRDGLPLSASTDFYHTQDFLEWRRRLKSLALRLAQPGRGSAEGCDFSIHF
SSFGDVACMAICSCQCPCPAAMAFCFLETLWWFTASYDTTCIGLASRPYAFLEFDSIIQKVKW
HFNYVSSSQMECSLEKIQEELKLQPPAVLTLEDVDANGVMNGHTPMHLEPAPNFRMEPVTA
LGILSLILNIMCAALNLIRGVHLAEHSLQDPRSWFCWLQTS

FIGURE 77

TGCTTCCTGGAGACCCTGTGGTGGATTACAGCTTCNTATGACACTACCTGCATTGGCNT
AGCCTCCAGGCCATACGCTTTCTTGAGTTGACAGCATCATTAGAAAGTGAAGTGGCATT
TTAACTATGTAAGTCCTNTCAGATGGAGTGCAGCTGGAAAAAATTCAAGGAGGAGCTCAAG
TTGCAGCCTCCAGCGTTCTCANTATGGAGGACACAGATGTGGCAAATGGGGT

FIGURE 78

CTCAGCGGCGCTTCCTCGTAGCGAGCCTAGTGGCGGGTGTTCGATTGAAACGTGAGCGCGA
CCCACCTAAAGAGTGGGAGCAAAGGGAGGACAGAGCCCTTAAAACGAGGCAGGGTGGTG
CCTGCCCTTAAGGGCGGGCGTCCGGACACTGTATCTGAGCCCCAGACTGCCCCGAGTT
TCTGTCGAGGCTCGAGGAAAGGCCCTAGGCTGGTCTGGTGCTGGCGGGCGCTT
CCTCCCCGCTCGTCCTCCCCGGGCCAGAGGCACCTCGGCTCAGTCATGCTGAGCAGAGTA
TGAAGGCACCTGACTACGAAGTGTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGC
GAGTGTATTATCAACACTCTGTTGCAACACTGTACATCCTCTGCCACATCTTCCTGAC
CCGCTCAAGAACGCTGCTGAGTTACACAGTGGATGATGAAGATGCCACCGTCAACAAGA
TTGCGCTCGAGCTGTGACCTTACCCGGCAATTGCCCTGGTGCTGTCCTGCTCCGCC
TTCTCCATCATCAGCAATGAGGTGCTGCTCCCTGGCAACTACTACATCCAGTGGCT
CAACGGCTCCCTACCATGGCCTGGAACCTTGTGTTCTTCTCCCAACCTGTCCTCA
TCTTCCTCATGCCCTTGCAATTCTCACTGAGTCTGAGGGCTTGCTGGCTCCAGAAAG
GGTGTCTGGGCCGGTCTATGAGACAGTGGTGATGTTGATGCTCCTCACTCTGCTGGTGCT
AGGTATGGTGGGTGGCATCAGCATTGTTGACAAGAACAGGCCAACAGAGAGTCAC
ATGACTTTGGGAGTACTATCTCCCTACCTACTCATGCACTCCTTCCTGGGTCTG
CTGCTCTGGTGTACTCCACTGGGTCTGGCCATGTTCTCCGTCAGTGGGAAGCTGCT
AGTCAAGCCCCGGCTGCTGGAGACCTGGAGGAGCAGCTGTACTGCTCAGCCTTGAGGAGG
CAGCCCTGACCCGCAAGGATCTGTAATCCTACTTCCTGCTGGCTGCCCTAGACATGGAGCTG
CTACACAGACAGGTCCTGGCTCTGCAGACACAGAGGGCTTGCTGGAGAACAGGGCGGAAGGC
TTCAGCCTGGCAACGGAACCTGGCTACCCCTGGCTATGCTGTGCTGCTGGTGCTGACGG
GCCTGCTGTGCTATTGTCAGGCTACCCACATCCTGGAGCTGCTCATCGATGAGGCTGCCATG
CCCCGAGGCATGCAGGGTACCTCTTAGGCCAGGTCTCCTCCAAGCTGGCTCCTTGG
TGCCGTCATTCAAGGTTGACTCATCTTACCTAATGGTGCTCAGTTGTCAGGCTCTATA
GCTCTCCACTCTCCGGAGCCTGGGCCAGATGGCACGACACTGCCATGACGAGATAATT
GGGAACCTGTGCTGCTCCTGGCTTAAGCTCAGCACTTCCTGCTCTCTCGAACCTGGG
GCTCACTCGCTTGACCTGCTGGTGACTTGGACGCTCAACTGGCTGGCAATTCTACA
TTGTGTTCCCTACAACGCAAGCTTGCAGGCCCTCACACACTCTGCTGGTGAGACCTTC
ACTGCAGCTGTGGGGCAGAGCTGATCCGGGCTTGGGCTGGACAGACTGCCGCTGCCGT
CTCCGGTTCCCCCAGGCATCTAGGAAGACCCAGCACCAG**TGA**CCTCCAGCTGGGGTGGGA
AGGAAAAAAACTGGACACTGCCATCTGCTGCCTAGGCCTGGAGGGAAAGGCCAAGGCTACTTGG
ACCTCAGGACCTGGAATCTGAGAGGGTGGTGCGAGAGGGAGCAGAGCCATCTGCACTATT
GCATAATCTGAGCCAGAGTTGGGACAGGACCTCCTGCTTTCCATACTTAACGTGGCCT
CAGCATGGGGTAGGGCTGGTGACTGGGCTAGCCCTGATCCCAAATCTGTTACACATCA
ATCTGCCCTACTGCTGTTCTGGGCATCCCCATAGCCATGTTACATGATTGATGTGCAAT
AGGGTGGGTAGGGCAGGGAAAGGACTGGGCCAGGGCAGGCTGGAGGATAGATTGCTCC
CTTGCTCTGGCCAGCAGAGCCTAAGCAGACTGTGCTATCCTGGAGGGCTTGGACCACTG
AAAGACCAAGGGGATAGGGAGGAGGAGGCTCAGCCATCAGCAATAAGTTGATCCCAGGGAA
AAAAAA

FIGURE 79

MEAPDYEVLSVREQLFHERIRECIISTLLFATLYILCHIFLTRFKPAEFTTVDDEDATVNK
IALELCFTLAIALGAVLLLPSIISNEVLLSLPRNYYIQWLNGSLIHGLWNLVFLFPNLSL
IFLMPFAYFFTESEGFAGSRKGVLGRVYETVVMLMLTLLVILGMVWVASAIVDKNKANRESL
YDFWEYYLPYLYSCISFLGVLLLLVCTPLGLARMFSVTGKLLVKPRLLEDLEEQLYCSAFEE
AALTRRICNPSCWLPLDMELLHRQVLALQTQRVLLEKRRKASAWQRNLGYPLAMLCLLVLT
GLSVLIVAIHILELLIDEAAMPRGMQGTSLGQVSFSKLGSFGAVIQVVLIFYLMVSSVVGFY
SSPLFRSLRPRWHDTAMTQIIGNCVCLVLSSALPVFSRTLGLTRFDLLGDFGRFNWLGNFY
IVFLYNAAFAGLTTLCLVKTFTAVERAELIRAFGLDRLPLPVSGFPQASRKTQHQ

FIGURE 80

GGCTGCCGAGGGAAGGCCCTGGTCTGGTCTGGCAGGGCCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGAAGC
ACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCAGTGTA
TTATATCAACACTTCTGTTGCAACACTGTACATCCTCTGCCACATCTCCTGACCCGCTTC
AAGAAGCCTGCTGAGTTACCACAGTGGATGATGAAGATGCCACCG

FIGURE 81

GACCGACCTTAAAGAGTGGGAGCAAAGGGAGGACAGAGCCTTTAAAACGAGGC GGTTGC
CTGCCCTTAAGGGCGGGCGTCGGACGACTGTATCTGAGCCCCAGACTGCCCGAGTTTC
TGTCGCAGGCTGCGAGGAAAGGCCCTAGGCTGGTCTGGT GCTTGGCGGCGGCTTCC
CCCCGTTGTCNTCCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGA
AGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGT
GTATTATATCAACACTTCTGTTGCAACACTGTACATCNTCTGCCACATCTCCTGACCCGC
TTCAAGAAGCCTGCTGAGTTACCACAGTGGATGATGAAGATGCCACCGTCAACAAGATTGC
GCTCGAGCTGTGCACCTTACCCCTGGCAATTGCCCTGGGTGCTGTCCTGCCCTTCT
CCATCATCAGCAATGAGGTGCTGCACTCCC

FIGURE 82

GATGTGCTCCTGGAGCTGGTGTGCAGTGTCTGACTGTAAGATCAAGTCCAAACCTGTTT
GGAATTGAGGAAACTCTCTTTGATCTCAGCCCTGGTGGTCCAGGTCTTC**ATG**CTGCTGT
GGGTGATATTACTGGTCCTGGCTCCTGTCAGTGGACAGTTGCAAGGACACCCAGGCCATT
ATTTCTCCAGCCTCCATGGACCACAGTCTCCAAGGAGAGAGTGACCCCTCACTGCAA
GGGATTTCGCTTCTACTCACCAAGAAAACAAATGGTACCATCGGTACCTGGGAAAGAAA
TACTAAGAGAAACCCCAGACAATATCCTTGAGGTTAGGAATCTGGAGAGTACAGATGCCAG
GCCCAGGGCTCCCTCTCAGTAGCCCTGTGCACTTGGATTTCTCAGAGATGGATTCC
TCATGCTGCCAGGCTAATGTTGAACCTCTGGCTCAAGTGATCTGCTCAC**TAG**GCCTCTC
AAAGCGCTGGGATTACAGCTTCGCTGATCCTGCAAGCTCCACTTCTGTGTTGAAGGAGAC
TCTGTGGTCTGAGGTGCCGGCAAAGGCAGTAACACTGAATAACTATTACAAGAA
TGATAATGTCCTGGCATTCTTAATAAAAGAACTGACTTCCAAAAAAAAAAAAAAA
AAA

FIGURE 83

MLLWVILLVLAPVSGQFARTPRPIIFLQPPWTTVFQGERVLTCKGFRFYSPQTKWYHRYLGKEILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDFSSEMGFPHAAQANVELLGSSDLLT

FIGURE 84

CAGAAGAGGGGGCTAGCTAGCTGTCTGCGGACCAGGGAGACCCCCCGGCCCGGTGT
 GAGGCGGCCTCACAGGGCCGGTGGCTGGCGAGCCGACGCCGGAGGAGGCTGTGAG
 GAGTGTGTGGAACAGGACCCGGGACAGAGGAACCA**ATG**GCTCCGCAGAACCTGAGCACCTTT
 GCCTGTTGCTGCTATAACCTCATCGGGCGGTGATTGCCGGACGAGATTCTATAAGATCTTG
 GGGGTGCCCTCGAAGTGCCTCTATAAAGGATATTAAAAAGGCCTATAGGAAACTAGCCCTGCA
 GCTTCATCCCACCGAACCCCTGATGATCCACAAGCCCAGGAGAAATTCCAGGATCTGGGTG
 CTGCTTATGAGGTTCTGTCAGATAGTGAGAAACGAAACAGTACGATACTTATGGTGAAGAA
 GGATTAAAAGATGGTCATCAGAGCTCCATGGAGACATTTTCACACTTCTTGGGATTT
 TGGTTTCATGTTGGAGGAACCCCTCGTCAGCAAGACAGAAATATTCCAAGAGGAAGTGATA
 TTATTGTAGATCTAGAACGTCACTTGGAAAGAAGTATATGCAGGAAATTGTGGAAGTAGTT
 AGAAACAAACCTGTGGCAAGGCAGGCTCCTGGCAAACGGAAGTGCAATTGTCGGCAAGAGAT
 GCGGACCACCCAGCTGGGCCCTGGCGCTTCCAAATGACCCAGGAGGTGGTCTGCGACGAAT
 GCCCTAATGTCAAACACTAGTGAATGAAGAACGAAACGCTGGAAGTAGAAATAGAGCCTGGGTG
 AGAGACGGCATGGAGTACCCCTTATTGGAGAAGGTGAGCCTCACGTGGATGGGAGCCTGG
 AGATTACGGTTCCGAATCAAAGTTGTCAAGCACCCATATTGAAAGGAGAGGAGATGATT
 TGTACACAAATGTGACAATCTCATTAGTTGAGTCACTGGTTGGCTTGAGATGGATATTACT
 CACTTGGATGGTCACAAGGTACATATTCCCGGGATAAGATCACCAAGGCCAGGAGCGAAGCT
 ATGGAAGAAAGGGGAAGGGCTCCCAACTTGTACAACAACAATATCAAGGGCTTTGATAA
 TCACTTTGATGTGGATTTCAAAAGAACAGTTAACAGAGGAAGCGAGAGAAGGTATCAA
 CAGCTACTGAAACAAGGGTCAGTGCAGAAGGTACAATGGACTGCAAGGATAT**TGA**GAGTG
 AATAAAATTGGACTTTGTTAAAATAAGTGAATAAGCGATATTATTATCTGCAAGGTTTT
 TTGTGTGTGTTTGTGTTTATTTCAATATGCAAGTTAGGCTTAATTGTTTATCTAATGA
 TCATCATGAAATGAATAAGAGGGCTTAAGAATTGTCCATTGCATTGGAAAAGAATGACC
 AGCAAAAGGTTACTAACCTCTCCCTTGGGATTTAATGTCTGGTGCTGCCGCTGAGT
 TTCAAGAATTAAAGCTGCAAGAGGACTCCAGGAGCAAAAGAAACACAATATAGAGGTTGGA
 GTTGTAGCAATTCAAAATGCCAAGTCTGTTTAAATACATTGTTA
 TTATTTTA

FIGURE 85

MAPQNLSTFCLLLYIGAVIAGRDFYKILGVPRSASIKDIKKAYRKLALQLHPDRNPDDPQ
AQEKFQDLGAAYEVLSDEKRKQYDTYGEEGLKDGHQS SHGDI FSHFFGDGF MFGGTPRQQ
DRNIPRGSDIIVDLEVTLEEYAGNFVEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPGRFQ
MTQEVCDEC PNVKLVNEERTLEVEIEPGVRDGMEYPFIGE GEPHVDGE PGDLRFRIKVVKH
PIFERRGDDLYTNVTISLVESL VG FEMDITHLDGHKVHISRDKITRPGAKLWKKGEGLPNFD
NNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQKVYNGLQGY

Important features:**Signal peptide:**

amino acids 1-22

Cell attachment sequence.

amino acids 254-257

Nt-dnaJ domain signature.

amino acids 67-87

Homologous region to Nt-dnaJ domain proteins.

amino acids 26-58

N-glycosylation site.

amino acids 5-9, 261-265

Tyrosine kinase phosphorylation site.

amino acids 253-260

N-myristoylation site.

amino acids 18-24, 31-37, 93-99, 215-221

Amidation site.

amino acids 164-168

FIGURE 86

TGGGACCAAGGAACCCCAGGGCCCCCGGTGGAGNGCCTAACAGGCCGGTGGNTGCGACCGAA
GCGGCAGGGCGGAGGAGGTTTGAGGATTTGGAACAGGACCCGGACAGAGGAACCATGGTT
CCGCAGAACNTGAGCACNTTGCCTGTTGNTGNTATACTTCATCGGGGCGGTGATTGCCGG
ACGAGATTTNTATAAGATTTGGGGTGCCTNGAAGTGCCTNTATAAAGGATATTAAAAAGG
CCTATAGGAAACTAGCCCTGCAGNTTATCCGACCGGAACCCTGATGATCCACAAGCCCAG
GAGAAATTCCAGGATTTGGGTGCTGCTTATGAGGTTNTGTCAGATAGTGAGAACGGAAACA
GTACGATAATTATGGTGAAGAAGGATTAAAAGATGGTNATCAGAGCTCCCATGGAGACATT
TTTCACACTNTTGGGGATTTGGTTTCATGTTGGAGGAACCCCTNGTCAGCAAGACAGA
AATATTCCAAGAG

FIGURE 87

GGCACGGAGGCGGCGGGCAGTCGCGGGATGCGCCCGGGAGCCACAGCCTGAGGCCCTCAGGT
 CTCTGCAGGTGTCGTGGAGGAACCTAGCACCTGCCATCCTCTCCCCAATTGCCACTCCA
 GCAGCTTAGCCCAGTGGAGGATGTGACCGGGACTGAGTCAGGAGCCCTCTGGAAGC**ATGG**
 AGACTGTGGTGATTGTTGCCATAGGTGTGCTGCCACCCTTTCTGGCTTCGTTGCAGCC
 TTGGTGCTGGTTGCAGGCAGCGCTACTGCCGGCCGAGACCTGCTGCAGCGCTATGATT
 TAAGCCCATTGTGGACCTCATTGGTGCCATGGAGACCCAGTCTGAGCCCTTGAGTTAGAAC
 TGGACGATGTCGTTATCACCAACCCCCACATTGAGGCCATTCTGGAGAAATGAAGACTGGATC
 GAAGATGCCTCGGGTCTCATGTCCCAGTGCATTGCCATCTGAAGATTGTCACACTCTGAC
 AGAGAAGCTTGGTGCATGACAATGGGCTCTGGGCAAGATGAAGACTTCAGCCAGTGTCA
 GCGACATCATTGTGGTGGCCAAGCGGATCAGCCCCAGGGTGGATGATGTTGTGAAGTCGATG
 TACCCCTCCGTTGGACCCAAACTCCTGGACGCACGGACACTGCCCTGCTCCTGTCTGTCAG
 TCACCTGGTGCCTGGTACAAGGAATGCCTGCCATCTGACGGGAGGCCTGGACTGGATTGACC
 AGTCTCTGTCGGCTGCTGAGGAGCATTGGAAGTCCTCGAGAAGCAGCCCTAGCTCTGAG
 CCAGATAAAGGCCCTCCAGGCCCTGAAGGCTTCCTGCAGGAGCAGTCTGCAATT**TAG**GCCT
 ACAGGCCAGCAGCTAGCCATGAAGGCCCTGCCGCATCCCTGGATGGCTAGCTTAGCCTT
 CTACTTTTCCTATAGAGTTAGTTGTTCTCACGGCTGGAGAGTTCAAGAAAATTGAGCCACCGTCT
 TAAAGCAGGAGATCCCCGTCACTTATGCCCTTTGCAGTTGCAAACGTGGCTGGTGAGT
 GGCAGTCTAATACTACAGTTAGGGAGATGCCATTCACTCTGCAAGAGGGAGTATTGAAAA
 CTGGTGGACTGTCAGCTTATTTAGCTCACCTAGTGTGTTCAAGAAAATTGAGCCACCGTCT
 AAGAAAATCAAGAGGTTCACATTAAATTAGAATTCTGGCCTCTCGATGGTCAGAATG
 TGTGGCAATTCTGATCTGCATTTCAAGAGGACAATCAATTGAAACTAAGTAGGGTTTC
 TTCTTGGCAAGACTTGACTCTCACCTGGCCTGTTCAAGGTTGGGTTGAAGCTGAGGAAC
 GGTCCCTGAGGCGTCTGGTCTCCTCCCTGCAGGTTGGGTTGAAGCTGAGGAAC
 ACAAAAGTTGATGATTCTTTTATCTTATGCCTGCAATTACCTAGCTACCACTAGGTG
 GATAGTAAATTATACTTATGTTCCCTCAAAAAAAAAAAAAAA

FIGURE 88

METVVIVAVLAVLATIFLASFAALVLVCRQRYCRPRDLLQRYDSKPIVDLIGAMETQSEPS
ELDDVVITNPHEAILENEDWIEDASGLMSHCIAILKICHTLTEKLVAMTMGSGAKMKT
VSIIIVVAKRISPRVDDVVKS MY PPLDPKL DARTTALLLSVSHLVLVTRNACHLTGGLDW
DQSL SAAEEHLEV LREA ALASEPDKGLPGPEGFLQE QSAI

FIGURE 89

GCTTCATTCTCCGACTCAGCTCCCACCCCTGGGCTTCCGAGGTGCTTCGCCGCTGTCC
CCACCACTGCAGCCATGATCTCCTAACGGACACGCAGAAAATTGGAATGGGATTAACAGGA
TTTGGAGTGTTCCTGTTGGAAATGATTCTCTTTGACAAAGCACTACTGGCTAT
TGGAAATGTTTATTGTAGCCGGCTTGGCTTGTAATTGGTTAGAAAGAACATTCA
GATCTCTCCAAAAACATAAAATGAAAGCTACAGGTTTCTGGGTGGTGTATTGTAGTC
CTTATTGGTTGGCCTTGATAGGCATGATCTCGAAATTATGGATTTCTCTGTT
GGGCTTCTTCCTGCGTGTGGCTTATTAGAAGAGTGCAGTCCTGGATCCCTC
CTAAATTTACCTGGAATTAGATCATTGTAGATAAAGTTGGAGAAAGCAACA
ATATGGTTAACAACA
AGTGAATTGAAGACTCATTTAAAATATTGTGTTATTATAAAGTCATTGAAGA
ATATTCA
GCACAAAATTAAATTACATGAAATAGCTTGTAAATGTTCTTACAGGAGTT
AAAACGTATAG
CCTACAAAGTACCAGCAGCAAATTAGCAAAGAAGCAGTGAAA
ACAGGCTCTACTCAAGTGA
ACTAAGAAGAAGTCAGCAAGCAA
ACTGAGAGAGGTGAAATCCATGTTAATGATGCTTAAGAA
ACTCTGAAGGCTATTGTGTTGTTCCACAATGTGCGAA
ACTCAGGCCATCCTAGAGAA
CTGTGGTGCCTGTTCTTTCTTTATTGAAGGCTCAGGAGCATCC
TAGGCATTGCT
TTTAGAAGTGTCCACTGCAATGGAAAAA
ATTTCCAGTTGCACTGTATCTCTGGAAAGTGA
TGCATGAATTGATTGGATTGTGTCATT
AAAGTATTAAAACCAAGGAAACCCCAATT
TG
ATGTATGGATTACTTTTTTNGCNCAGGGCC

FIGURE 90

MISLTDTQKIGMGLTGFGVFFLFFGMILFFDKALLAIGNVLFVAGLA
FVIGLERTFRFFFQK
HKMKATGFFLGGVFVVLIGMIFEIYGFLLFRGFFPVVVGFI
RRVPVLGSLLNLPGI
RSFVDKVGESNNMV

Important features:

Transmembrane domains:

amino acids 12-30 (typeII), 33-52, 69-89 and 93-109

N-myristoylation sites.

amino acids 11-16, 51-56 and 116-121

Aminoacyl-transfer RNA synthetases class-II protein.

amino acids 49-59

FIGURE 91

GAAGACGTGGCGGCTCTGCCCTGGCTGTTCCCGGCTTCATTCTCCGACTCAGCTTCCC
ACCNTGGGCTTCCGAGGTGCTTCGCCGCTGTCCCCACCACTGCAGCCATGATCTCCTTAA
CGGACACGCAGAAAATTGGAATGGGATTAACCGGATTGGAGTGTTCCTGTTGGAA
ATGATTCTCTTTTGACAAAGCACTACTGGCTATTGAAATGTTTATTGTAGCCGGCTT
GGCTTTGTAATTGGTTAGAAAGAACATTTCAGATTCTTCCAAAAACATAAAATGAAAG
CTACAGGTTTTCTGGGTGGTGTATTGTAGTCCTATTGGTTGGCCTTGATAGGCATG
ATCTCGAAATTATGGATTTCTCTTGTTC

FIGURE 92

GGCACGAGGCTGAACCCAGCCGGCTCATCTCAGCTCTGGTTCTAAGTCCATGTGCCAAA
 GGCTGCCAGGAAGGAGACGCCCTCCTGAGTCCTGGATCTTCTTCCTCTGGAAATCTTGA
 CTGTGGTAGTTATTATTCTGAATAAGAGCGTCCACGCATC**ATG**GACCTCGCGGGACTGC
 TGAAGTCTCAGTCAGTCAGTCTGACCCTGGTCTCTGCTACGTCTTATTGCCTCAGGGCTAATC
 ATCAACACCATTCACTCTCAGTCTTCACTCTCCTCTGGCCCATTAAACAAGCAGCTTCCGAA
 GATCAACTGCAGACTGTCCTATTGCATCTCAAGCCAGCTGGTATGCTGCTGGAGTGGTGGT
 CGGGCACGGAATGCACCATCTCACGGACCCGCGCCTACCTCAAGTATGGAAAGGAAAAT
 GCCATCGTGGTCTCAACCACAAGTTGAAATTGACTTCTGTGTGGCTGGAGCCTGTCCGA
 ACGCTTGGCTGTTAGGGGCTCCAAGGCCTGGCAAGAAAGAGCTGGCCTATGTCCAA
 TTATCGGCTGGATGTGGTACTTCACCGAGATGGTCTTCTGTTCGCGCAAGTGGGAGCAGGAT
 CGCAAGACGGTGCACCGAGTTGCAGCACCTCCGGACTACCCCCGAGAAGTATTTTCCCT
 GATTCACTGTGAGGGCACACGGTCACGGAGAAGAACATGAGATCAGCATGCAGGTGGCCC
 GGGCCAAGGGCTGCCTCGCCTCAAGCATCACCTGTTGCCACGAACCAAGGGCTCGCCATC
 ACCGTGAGGAGCTTGAGAAATGTAGTTCAGCTGTATATGACTGTACACTCAATTTCAGAAA
 TAATGAAAATCCAACACTGCTGGAGTCCTAAACGAAAGAAATACCATGCAGATTGTATG
 TTAGGAGGATCCACTGGAAGACATCCCTGAAGACGATGACGAGTGCTCGGCCTGGCTGCAC
 AAGCTTACCAAGGAGAAGGATGCCCTTCAGGAGGAGTAACAGGACGGGACCTTCCAGA
 GACGCCATGGTCCCCCCCCGGCGGCCCTGGACCCCTCGTAACGGCTGTTGGGCTCGC
 TGGTGCCTACCCCTTCTTCAGTCCTGGTCAGCATGATCAGGAGCGGTCTTCCCTGACG
 CTGGCCAGCTTCATCCTCGTCTTGTGGCTCCGTGGAGTTGATGGATGATTGGTGT
 GACGGAAATTGACAAGGGCTCGCCTACGGCAACTCTGACAGCAAGCAGAAACTGAATGACT
GACTCAGGGAGGTGTCACCATCCGAAGGGAACCTGGGAACGGCTCTGCATATCCT
 CCTTAGTGGACACGGTACAAAGGCTGGTGAGCCCTGCTGGCACGGCGGAAGTCACGA
 CCTCTCCAGCCAGGGAGTCTGGTCTCAAGGCCGGATGGGAGGAAGATGTTGTAATCTT
 TTTTCCCCATGTGCTTAGTGGCTTGGTTCTTGTGAGTGTGTGAGAATGGC
 TGTGGTGAGTGTGAACCTTGTCTGTGATCATAGAAAGGGTATTTAGGCTGCAGGGAG
 GGCAGGGCTGGGACCGAAGGGACAAGTCCCCTTCATCCTTGGTGTGAGTTCTGT
 AACCCCTGGTTGCCAGAGATAAAAGTGAAAAGTGTAGGTGAGATGACTAAATTATGCCTC
 CAAGAAAAAAATTAAAGTGTCTTCTGGTCAAAAAAAAAAA

FIGURE 93

MDLAGLLKSQFLCHLVFCYVFIASGLIINTIQLFTLLLWPI NKQLFRKINCRLSYCISSQLV
MLLEWWSGTECTIFTDPRAYLKYGKENAIVVLNHKEIDFLCGWSLSERFGLGGSKVLAKK
ELAYVPIIGWMWYFTEMVFCSRKWEQDRKTVATSLQHLRDYPEKYFFLIHCEGTRFTEKHE
ISMQVARAKGLPRLKHLLPRTKGFAITVRSLRNVSAVYDCTLNFRNNENPTLLGVNGKK
YHADLYVRRIPLEDIPEDDDECASAWLHKLYQEKD AFQEEYYRTGTFPETPMVPPRPWTLVN
WLFWASLVLYPFFQFLVSMIRSGSSLTLASFILVFFVASVGVRWMIGVTEIDKGSAYGNSDS
KQKLND

FIGURE 94

CTGAGGC GGCGGTAGC**ATG**GAGGGGGAGAGTACGT CGGCGGTGCTCTCGGGCTTGTGCTCG
 GCGCACTCGCTTCCAGCACCTAACACACGGACTCGGACACGGAAGGTTTCTTCTGGGAA
 GTAAAAGGTGAAGCCAAGAACAGCATTACTGATTCCAAATGGATGATGTTGAAGTTGTTA
 TACAATTGACATT CAGAAATATATTCCATGCTATCAGCTTTAGCTTTATAATTCTTCAG
 GCGAAGTAAATGAGCAAGCACTGAAGAAAATATTCAAATGTCAAAAAGAATGTGGTAGGT
 TGGTACAAATTCCGTCGT CATT CAGATCAGATCATGACGTTAGAGAGAGGCTGCTCACAA
 AAAC TTGCAGGAGCATTTCAAACCAAGACCTGTTCTGCTATT AACACCAAGTATAA
 TAACAGAAAGCTGCTCTACTCATCGACTGGAACATT CCTTATATAAACCTCAAAAAGGACTT
 TTTCACAGGGTACCTTAGTGGTGCCAATCTGGGCATGTCTGAACAACTGGTTATAAAC
 TGTATCAGGTTCTGTATGTCCACTGGTTAGCCGAGCAGTACAAACACACAGCTCTAAAT
 TTTTGAGAAGATGGATCCTAAAGGAGGTACATAAGATAATGAAATGTATGCTTCATTA
 CAAGAGGAATTAAAGAGTATATGCAAAAAGTGGAAAGACAGTGAACAAAGCAGTAGATAAACT
 AGTAAAGGATGTAAACAGATTAAAACGAGAAATTGAGAAAAGGAGAGGAGCACAGATT CAGG
 CAGCAAGAGAGAAGAACATCCAAAAGACCCCTCAGGAGAACATTTCCTTCAGGCATTA
 CGGACCTTTTCCAAATTCTGAATTCTCATT CATGTGTTATGCTTTAAAAAATAGACA
 TGTTCTAAAAGTAGCTGTA ACTACAACCACCATCTCGATGTAGTAGACAATCTGACCTAA
 TGGTAGAACACACTGACATT CCTGAAGCTAGTCCAGCTAGTACACCACAAATCATTAAGCAT
 AAAGCCTTAGACTAGATGACAGATGGCAATTCAAGAGATCTGGTTGTTAGATACACAAGA
 CAAACGATCTAAAGCAAATCTGGTAGTAGTAACCAAGATAAGCATCCAAAATGAGCAGCC
 CAGAAACAGATGAAGAAATTGAAAAGATGAAGGGTTGGTGAATATT CACGGCTCCTACA
 TTT**TGA**TCCTTTAACCTTACAAGGAGATT TTTTATTGGCTGATGGTAAAGCCAAACAT
 TTCTATTGTTTACTATGTTGAGCTACTTGCAGTAAGTTCACTTGTTTACTATGTT CAC
 CTGTTGCAGTAATACACAGATAACTCTTAGTGCATTACTCACAAAGTACTTTCAAAC
 ATCAGATGCTTTATTCCAAACCTTTT CACCTTCACTAAGTTGTTGAGGGGAAGGCT
 TACACAGACACATTCTT TAGAATTGGAAAAGT GAGACCAGGCACAGTGGCTCACACCTGTAA
 TCCCAGCACTAGGGAAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCC
 TGGGCAACGTATTGAGACCATGTCTATTAAAAAATGGAAAAGCAAGAATAGCCTTAT
 TTTCAAAATATGGAAAGAAATTATGAAAATTATCTGAGTCATTAAAATTCTCCTTAAG
 TGATACTTTT TAGAAGTACATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCA
 ATAAATTGCAAAACATCATCTAAAATTAAAAAAAAAAAAAAA

FIGURE 95

MEGESTSAVLSGFVLGALAFQHLNTDSDEGVKGEAKNSITDSQMDDVEVVYTIDIQ
KYIPCYQLFSFYNSSGEVNEQALKKILSNVKKNVGWYKFRRHSDQIMTFRERLLHKNLQEHE
FSNQDLVFLLLTPSIITESCSTHRLEHSLYKPQKGLFHRVPLVVANLGMSEQLGYKTVSGSC
MSTGFSRAVQTHSSKFFED GSLKEVHKINEMYASILQEELKSICKVEDSEQAVDKLVKDVN
RLKREIEKRRGAQIQAAREKNIQKDPQENIFLCQALRTFPNSEFLHSCVMSLKNRHVS KSS
CNYNHHLDVVVDNLTL MVEHTDIPEAS PASTPQIIKHKA LD LDDR WQFKRS RLL DT QDKRS KA
NTGSSNQDKASKMSSPETDEEIEKMKG FGEYSRSPTF

FIGURE 96

GGCACAGCCGCGCGGGAGGGCAGAGTCAGCCGAGCCAGTCCAGCCGGACGAGCGGACCAGCGCAGGGCAGC
 CCAAGCAGCGCGAGCGAACGCCGCCGCCACACCCCTGCGGTCCCCGCCCTGCCACCCCTTCCCT
 CCTTCCCCCGCTCCCCGCCCTGCCGGCCAGTCAGCTGCCGGGTTCGCTGCCCGCAAACCCCGAGGTACCCA
 GCCCGCGCCCTGCTCTCCCTGGGCCGCCGCCCTCCACGCCCTCCTCTCCCTGGCCGCCCTGGCAC
 GGGGACCGTTGCCTGACCGAGGCCAGCTACTTTGCCCGCGCTCTCCCTGCCCTGCTGCCCTTCCAC
 CAACTCCAACCTCCTCTCCCTCCAGCTCACTCGTAGTCCCCGACTCCGCCAGGCCCTGCCCGCTGCCCTAG
 CGCCGCTTCCCCTCCGGTCCCAAAGGTGGAACCGCGTCCGCCGGGCCACC**ATG**GCACGGTCGGCTGCC
 CGCGCTTCTGCAACCTGGCAGTGTCAAGGCCCGCGTGGCTGGCAGGCTCAAGTCGAAAAGTTGCTCGG
 AAGTGCACGTCTTACGTGTCACAAAGGCTCAACAAAGAACGATGCCCTCCACAGAGATCAACGGTGATCAT
 TTGAAGATCTGTCCTCAGGGTCTACCTGCTGCTCTCAAGAGATGGAGGAGAAGTACAGCCTGCAAAGTAAGA
 TGATTTCAAAAGTGTGGTCAGCGAACAGTGAATCATTTGCAAGCTGTCTTGCTTCACGTTACAAGAAGTTG
 ATGAATTCTCAAAGAACTACTTGAAGAAATCCGTAATGATATGTTGTGAAGACATATGGCCAT
 TTATACATGCAAAATTCTGAGCTATTTAAAGATCTTCGTAAGAGTTGAAACGTTACTACGTGGTGGAAATGT
 GAACCTGGAAGAAATGCTAAATGACTCTGGGCTCGCCTGGAGCGGATGTTCCGCTGGTGAACTCCAGT
 ACCACTTACAGATGAGTATCTGGAATGTGTGAGCAAGTATACGGAGCAGCTGAAGCCCTCGGAGATGTCCT
 CGCAAATTGAAGCTCCAGGTTACTCGTGTGTTGAGCAGCCGTAATTGCTCAAGGTTAGCGGTTGCCGG
 AGATGTCGTGAGCAAGGTCTCGTGGTAACCCACAGGCCAGTGTACCCATGCCCTGTTGAAGATGATCTACT
 GCTCCCACTGCCGGGGTCTCGTACTGTGAAGCCATGTTACAACACTGCTCAAACATCATGAGAGGCTGTTG
 GCCAACCAAGGGATCTGATTTGAATGGAACAATTTCATAGATGCTATGCTGATGGTGGCAGAGAGGCTAGA
 GGGTCCTTCAACATTGAATCGTCATGGATCCCATCGATGTGAAGATTCTGATGCTATTATGAACATGCAGG
 ATAATAGTGTCAAGTGTCTCAGAAGGTTTCAGGGATGTGGACCCCCAAGCCCTCCAGCTGGACGAATT
 TCTCGTCCATCTGAAAGTGCCTTCAGTGCTCGCTCAGACCACATCACCCGAGGAACGCCAACACAGC
 AGCTGGCACTAGTTGGACCGACTGGTACTGATGTCAGGAGAACTGAAACAGGCAAGAAATTCTGGCCT
 CCCTCCGAGCAACGTTGCAACGATGAGAGGATGGCTGCAGGAAACGGAATGAGGATGACTGTTGGAATGGG
 AAAGGCAAAAGCAGGTACCTGTTGCAAGGAAATGGATTAGCCAACCAGGGCAACAACCCAGAGGTCCA
 GGTTGACACCAGCAAACAGACATACTGATCCCTCGTCAAATCATGGCTCTCGAGTGTGACCAAGGATGA
 AGAATGCATACAATGGAACGACGTGGACTTCTTGTATCAGTGTGAAAGTAGTGGAGAAGGAAGTGGAAAGT
 GGCTGTGAGTATCAGCACTGCTGCTGCTGGGACAGGCCACTGACCATGCTGGGAAGAGTGCCAATG
 GAAAGCCGACAGTGCTGGTGTCCGTCCTGGGGCACAGGCCACTCTCACTGTCTCTGCATTTGTTCTGG
 TTATGCAGAGAGATGGAGA**TAA**TTCTCAAACCTGAGAAAAAGTGTTCATCAAAAGTTAAAAGGCCACAGTT
 ATCACTTTCTACCATCCTAGTGACTTGCTTTAAATGAATGGACAACATGTACAGTTTACTATGTGGC
 CACTGGTTAAGAAGTGTGACTTGTTCTCATTGAGTTGGAGGAAAGGGACTGTGCATTGAGTTGGT
 TCCTGCTCCCCAACCATGTTAAACAGTGGCTAACAGTGTAGGTACAGAACTATAGTTGTCATTTGTA
 TTTTATCACTTATTATTTGTTGATGTTTCTCATTGTTGTTGGGGTTTTTCAACTGTGATCT
 CGCTTGTGTTCTACAAGCAAACCAAGGGCCCTTCTGGCACGTAACATGTACGTTAGTGTGCAATTAAATA
 GCTGTACAGAACAGGTTTATTTATGTTATCTTATTAAAAGAAAAAGCCCAAAAGC

FIGURE 97

MARFGLPALLCTLAVLSAALLAAELSKSKCSEVRRLYVSKGFNKNDAPLHEINGDHLKICPQ
GSTCCSQEMEEKYSIQLSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSLNDF
VKTYGHLYMQNSELFKDLFVELKRYVVGNVNLEEMLNDFWARLLERMFRFLVNSQYHFTDEY
LECVSKYTEQLPKPGDVRKLKLQVTRAFVAARTFAQGLAVAGDVSKVSVNPATAQCTHAL
LKMIYCSCSHCRGLVTVKPCNYCSNIMRGCLANQGDLDFEWNNFIDAMLMVAERLEGPFNIES
VMDPIDVKISDAIMNMQDNSVQVSQKVFOCGCGPPKPLPAGRISRSISESAFSARFRPHHPEE
RPTTAAGTSLDRLVTDVKEKLKQAKKFWSLPSNCNDERMAAGNGNEDDCWNGKGKSRYLF
AVTGNGLANQGNNPEVQVDTSKPDILILRQIMALRVMTSKMKNAYNGNDVDFFDISDESSGE
GSGSGCEYQQCPSEFDYNATDHAGKSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

FIGURE 98

CTGCCCTCAAATGGAACGCTGGCCTGGACTAAAGCATAGACCACCAGGCTGAGTATCCT
GACCTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTCCATTATATTCTTCAA
GCAACTTACAGCTGCACCGACAGTTGCGATGAAAGTTCTAATCTCTCCCTCCTCCTGTTGC
TGCCACTAATGCTGATGTCCATGGCTCTAGCAGCCTGAATCCAGGGGTCGCCAGAGGCCAC
AGGGACCGAGGCCAGGCTCTAGGAGATGGCTCCAGGAAGGCAGCCAAGAATGTGAGTGCAA
AGATTGGTTCTGAGAGCCCCGAGAAGAAAATTGACAGTGTCTGGGCTGCCAAAGAAGC
AGTGCCCTGTGATCATTCAAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACCACAGA
AAGCCAAACAAGCATTCCAGAGCCTGCCAGCAATTCTCAAACAATGTCAGCTAAGAAGCTT
TGCTCTGCCTTGTAGGAGCTCTGAGCGCCACTCTCCAATTAAACATTCTCAGCCAAGAA
GACAGTGAGCACACCTACCAGACACTCTTCTTCTCCACCTCACTCTCCACTGTACCCACC
CCTAAATCATTCCAGTGCTCTCAAAAAGCATGTTTTCAAGATCATTTGTTGCTCTC
TCTAGTGTCTTCTTCTCGTCAGTCTTAGCCTGTGCCCTCCCTACCCAGGCTTAGGCTT
AATTACCTGAAAGATTCCAGGAAACTGTAGCTCCTAGCTAGTGTCAATTAAACCTAAATGC
AATCAGGAAAGTAGCAAACAGAAGTCAATAATTTTAAATGTCAAAAAAAAAAAAAAAA

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FIGURE 99

MKVLISLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRR
KFMTVSGLPKKQCPDCDFKGNVKTRHQRHHRKPNKHSRACQQFLKQCQLRSFALPL

FIGURE 100

AATGGCTGTCTTAGTACTCGCCTGACAGTTGTCTGGACTGCTTGCTTATTCCCTGACCT
GCTATGCAGACGACAAACCAGACAAGCCAGACGACAAGCCAGACGACTCGGGCAAAGACCCA
AAGCCAGACTTCCCCAAATTCTTAAGCCTCCTGGCACAGAGATCATGAGAATGCAGTCGA
GTTCATCCTCCGCTCCATGTCCAGGAGCACAGGATTATGGAATTGATGATAATGAAGGAA
AACATTCATCAAAGTGACATCCTCAGGACACACCCATGTGGCTCCTGGACAATCCAAGAGCA
GCCAAATCCTGCTTCCAGTTGGCTCCACAAGTCCTCCAGGACAGAGCCCTCAAAGCAAC
TCCCACGAGTTCTCAGGATTCAAGGCTCTGGCTTCAACCAACAGAACTCATTGAACACC
CTGACTGCATTTGCTTTAGAAAGTTAGAATAATGGCGCTTGGATCACATAGTTG
ATGGAGAGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 101

MAVLVLRLTVVLGLLVLFLTCYADDKPDKPDDKPDGKDPDFPKFLSLLGTEIIENAVE
FILRSMSRSTGFMEFDDNEGKHSSK

FIGURE 102

GGACGCCAGCGCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTCCCCAGCGGAAGCACAGCT
CAGAGCTGGTCTGCCATGGACATCCTGGTCCACTCCTGCAGCTGCTGGTGTGCTTCTAC
CCTGCCCTGCACCTCATGGCTCTGCTGGCTGCTGGCAGCCCCTGTGCAAAGCTACTTCC
CCTACCTGATGCCGTGCTGACTCCAAGAGCAACCGCAAGATGGAGAGCAAGAACGGAG
CTCTTCAGCCAGATAAAGGGGCTTACAGGAGCCTCCGGAAAGTGGCCTACTGGAGCTGGG
CTGCGAACCGGAGCCAACTTCAGTTCTACCCACCAGGCTGCAGGGTCACCTGCCTAGACC
CAAATCCCCACTTGAGAAGTTCCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATAT
GAGCGGTTGTGGTGGCTCCTGGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGT
GGTGGTCTGCACTCTGGTGTGCTCTGTGCAGAGCCAAGGAAGTCCTGCAGGAGGTCC
GGAGAGTACTGAGACCAGGGAGGTGTGCTCTGGAGACATGTGGCAGAACCATATGGA
AGCTGGGCCTTCATGTGGCAGCAAGTTCGAGGCCACCTGAAACACATTGGGATGGCTG
CTGCCTCACCAAGAGAGACCTGGAAGGATCTTGAGAACGCCAGTTCTCCGAAATCCAATGG
AACGACAGCCCCCTCCCTGAAGTGGCTACCTGTTGGCCCCACATCATGGAAAGGCTGTC
AAACAATCTTCCAAGCTCCAAGGCACCTTGCTCCTCCCCAGCCTCCAATTAGAACAA
AGCCACCCACCAGCCTATCTATCTTCACTGAGAGGGACCTAGCAGAATGAGAGAACATT
CATGTACCACCTACTAGTCCCTCTCCCCAACCTCTGCCAGGGCAATCTTAACCTCAATC
CCGCCTCGACAGTAAAAAGCTACTTCTACGCTGACCCAGGGAGGAAACACTAGGACCC
TGTTGTATCCTCAACTGCAAGTTCTGGACTAGTCTCCCAACGTTGCCCTCCAAATGTTGTC
CCTTCCCTCGTTCCCATGGTAAAGCTCCTCTGCTTCCCTGTGAGGCTACACCCATGCGT
CTCTAGGAACGGTCACAAAAGTCATGGTGCCTGCATCCCTGCCAAGCCCCCTGACCCCT
CTCCCCACTACCACCTCTCCTGAGCTGGGGCACCAGGGAGAATCAGAGATGCTGGGAT
GCCAGAGCAAGACTCAAAGAGGCAGAGGTTTGTCTCAAATATTTTAATAATAGACGA
AACACAG

FIGURE 103

MDILVPLLQLLVLLTLPLHLMALLGCWQPLCKSYFPYLMAVLTPKSNRKMESKKRELFSQL
KGLTGASGKVALLELGCGTGANFQFYPPGCRVTCLDPNPHFEKFLTKSMAENRHLQYERFVV
APGEDMRQLADGSMDVVVCTLVLCVQSPRKVLQEVRVLRPGGVLFFWEHVAEPYGSWAFM
WQQVFEPTWKHIGDGCLTRETWKDLENAQFSEIQMERQPPPLKWLPGPHIMGKAVKQSFP
SSKALICSFPSLQLEQATHQPIYIPLRGT

FIGURE 104

GTGGGATT TATTGAGTGCAAGATCGTTCTCAGTGGTGGGAAGTTGCCTCATCGCAGG
 CAGATGTTGGGCTTGTCCGAACAGCTCCCCTGCCAGCTCTGTAGATAAGGGTTAAAA
 ACTAATATTATATGACAGAAGAAAAG**TG**TCAATTCCGTAAAGTAAACATCATCATCTTGG
 TCCTGGCTGTTGCTCTTACTGGTTGCACCATAACTCCTCAGCTGAGCAGTTG
 TTAAGGAATGAGGTTACAGATTAGGAATTGTAGGGCCTCAACCTATAGACTTGTCCAAA
 TGCTCTCCGACATGCAGTAGATGGGAGACAAGAGGGAGATTCCGTGGTCATCGCTGCATCTG
 AAGACAGGCTTGGGGGCCATTGCAGCTATAAACAGCATTAGCACAACACTCGCTCCAAT
 GTGATTTCCTACATTGTTACTCTCAACAATACAGCAGACCATCTCCGGCTGGCTAACAG
 TGATTCCCTGAAAAGCATCAGATACAAATTGTCAATTGACCTAAACTTTGGAAGGAA
 AAGTAAAGGAGGATCCTGACCAGGGGAATCCATGAAACCTTAACCTTGCAAGGTTCTAC
 TTGCCAATTCTGGTCCCAGCGCAAAGAAGGCCATATACATGGATGATGTAATTGTGCA
 AGGTGATATTCTGCCCCTTACAATACAGCACTGAAGCCAGGACATGCAGCTGCATTTCAG
 AAGATTGTGATTGCCTACTAAAGTTGTACCGTGAGCAGGAAACCAGTACAATTAC
 ATTGGCTATCTGACTATAAAAGGAAAGAATTGTAAGCTTCCATGAAAGCCAGCACTG
 CTCATTAATCCTGGAGTTTGCAACCTGACGGAATGGAAACGACAGAATATAACTA
 ACCAACTGGAAAAATGGATGAAACTCAATGTAGAAGAGGGACTGTATAGCAGAACCTGGCT
 GGTAGCATCACACACCTCCTGCTTATCGTATTTCACAGCACTTACCATCGATCC
 TATGTGGAATGTCGCCACCTGGTCCAGTGCTGGAAAACGATATTCACCTCAGTTGAA
 AGGCTGCCAAGTTACTCCATTGGAATGGACATTGAAAGCCATGGGAAGGACTGCTTCATAT
 ACTGATGTTGGAAAAATGGTATATTCCAGACCCAACAGGAAATTCAACCTAATCCGAAG
 ATATAACCGAGATCTCAAACATAAAG**TG**AACAGAATTGAACTGTAAGCAAGCATTCTCAG
 GAAGTCCTGGAAGATAGCATGCATGGGAAGTAACAGTTGCTAGGCTCAATGCCTATCGGTA
 GCAAGCCATGGAAAAAGATGTGTAGCTAGGTAAAGATGACAAACTGCCCTGTGGCAGTC
 AGCTTCCAGACAGACTATAGACTATAAAATATGTCCTCATGCCCTACCAAGTGTGTTCTT
 ACTACAATGCTGAATGACTGGAAAGAAGAACTGATATGGCTAGTCAGCTAGCTGGTACAGA
 TAATTCAAAACTGCTGTTGGTTAATTGTAACCTGTGGCCTGATCTGTAATAAAACTT
 ACATTTTC

FIGURE 105

MSFRKVNIILVLAVALFLLVLHHNFLSLLRNEVTDSGIVGPQPIDFVPNALRHAVDGR
QEEIPVIAASEDRGGAIAAINSIQHNTRSNVIFYIVTLNNNTADHLRSWLNSDSLKSIRYK
IVNFDPKLLEGKVKEPDQGESMKPLTFARFYLPILVPSAKKAIYMDDDViVQGDILALYNT
ALKPGHAAAFSEDCDSAStKVViRGAGNQNYIGYLDYKKERIRKLSMKASTCSFNPGVFVA
NLTEWKRNITNQLEKWMKLNVEEGLYSRTLAGSiTTPLLIVFYQQHSTiDPMWNVRHLGS
SAGKRYSPQFVKAAKLLHWNGHLKPWGRTASYTDVWEKWYiPDPtgfNLIRRyTEiSNiK

FIGURE 106

TGGTTTTGCCCTAAATTCCCTCAGCTTGAGCAGTTGTTAAGGAATGAGGTACAGATT
CAGGAATTNTAGGN CCTCAACCTNTAGANTTGTCCCAAATGTTCTCCGACATGCAGTAGAT
GGGAGACAAGAGGAGATT CCGTGGTCATCGCTGCATNTGAAGACAGGCTGGGGGGCCAT
TGCAGCTATAAACAGCATT CAGCACAAACACTCGNTCCAATGTGATT TCTACATTGTTACTC
TCAACAATACAGCAGACC ATNTCCGGT CCGNTCAACAGT GATTCCCTGAAAAGCATCAGA
TACAAAATTGTCAATT TGACCCTAAACTTTGGAAGGAAAAGTAAAGGAGGATCCTGACCA
GGGGGAATCCATGAAACCTTAACCTTGCAAGGTTCTACTTGCCAATTCTGGTTCCCAGCG
CAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTGCCCTTAC
AATACAGCACTGAAGCCAGGACATGCAGCTGCATTTCAGAAGATTGTGATT CAGCCTCTAC
TAAAGTTGTCACTCCGTGGAGCAGGAAA

FIGURE 107

CGACGCTCTAGCGGTTACCGCTGCGGGCTGGCTGGCGTAGTGGGCTGCGCGGCTGCCACG
 GAGCTAGAGGGCAAGTGTGCTCGGCCAGCGTCAGGGAACGCAGGCGGCCAGACAACGGGC
 TGGGCTCCGGGCCTGCGCGCGCTGAGCTGGCAGGGCGGGTCGGGCGCGGGCTGCA
 TCCGCATCTCCTCCATCGCCTGCAGTAAGGGCGGCCGGCAGCCTTGAGGGAACGACT
 TGTCGGAGCCCTAACCAAGGGGTGCTCTGAGCCTGGGATCCCCGGAGCGTCACATCACT
 TTCCGATCACTCAAAGTGGTAAAAACTAATATTATATGACAGAAGAAAAGATGTCATT
 CCGTAAAGTAAACATCATCATCTGGCCTGGCTGTTGCTCTTCTTACTGGTTTGAC
 CATAACTCCTCAGCTTGAGGCAGTTGTTAAGGAATGAGGTTACAGATTAGGAATTGAG
 GGCCTCAACCTATAGGACTTGTCCAAATGCTCTCGACATGCAGTAGATGGGAGACAAGA
 GGAGATTCTGTGGTCATCGCTGCATCTGAAGACAGGCTTGGGGGCCATTGCAGCTATAA
 ACAGCATTCAGCACAACACTCGCTCCAATGTGATTTCTACATTGTTACTCTCAACAAATACA
 GCAGACCCTCTCCGGTCTGGCTCAACAGTGATTCCCTGAAAAGCATCAGATAACAAATTG
 TCAATTGACCCCTAAACTTGGAAAGGAAAAGTAAAGGAGGATCCTGACCAGGGGAATCC
 ATGAAACCTTAAACCTTGCAAGGTTACTTGCCAATTCTGGTTCCCAGCGCAAAGAAGG
 CCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTGCCCTTACAATACAGCA
 CTGAAGCCAGGACATGCAGCTGCATTTCAGAAGATTGTGATTGCAGCCTCTACTAAAGTTGT
 CATCCGTGGAGCAGGAAACCAAGTACAATTACATTGGCTATCTGACTATAAAAGGAAAGAA
 TTCGTAAGCTTCCATGAAAGCCAGCACTGCTCATTAACTTGAGTTTGCAAC
 CTGACGGAATGGAAACGACAGAAATATAACTAACCAACTGGAAAATGGATGAAACTCAATGT
 AGAAGAGGGACTGTATAGCAGAACCCCTGGCTGGTAGCATCACAAACACCTCCTGCTTATCG
 TATTTATCAACAGCACTTACCATCGATCCTATGTGGAATGTCCGCCACCTGGTTCCAGT
 GCTGGAAAACGATATTCACCTCAGTTGAAAGGCTGCCAGTTACTCCATTGGAATGGACA
 TTTGAAGCCATGGGAAGGACTGCTTCAATACTGATGTTGGGAAAATGGTATATTCCA
 GACCCAAACAGGCAAATTCAACCTAACCGAAGATACCGAGATCTCAAACATAAAAGTGAAA
 CAGAATTGAACTGTAAGCAAGCATTCTCAGGAAGTCCCTGGAAGATAGCATGCGTGGGAAG
 TAACAGTTGCTAGGCTCAATGCCATTGCTCGGTAGCAAGCCATGGAAAAGATGTGTCAGCTAG
 GTAAAGATGACAAACTGCCCTGCTGGCAGTCAGCTCCAGACAGACTATAGACTATAAT
 ATGTCCTCCATCTGCCATTACCAAGTGTGTTCTACTACAATGCTGAATGACTGGAAAGAAGAA
 CTGATATGGCTAGTCAGCTAGCTGGTACAGATAATTCAAAACTGCTGTTGGTTAATT
 GTAACCTGTGGCCTGATCTGTAATAAAACTACATTTCATAGGTAAAAAAAAAAAAAA
 AAAAAA

FIGURE 108

CTGCAGGTAGACATCTCACTGCCAGGAATCACTGAGCGTGCAGACAGCACAGCCTCCTCT
GAAGGCCGGCCATACCAGAGTCCTGCCTCGGCATGGGCCTCACCATTGAGGCAGCTCCACTG
TCTGTGCTGGTCTGAGGGTGCCTGTC**ATG**GGGCAGCCATCTCCCAGGGGCCCTCATC
GCCATCGTCTGCAACGGTCTCGTGGCTTCTGCTGCTGCTCTGGTATCCTCTGCTG
GGCCTGCCATTCTCGTCTGCCGACGTTGACTCTCTGAATCCAGTCCAACTCCAGCCC
TGGCCCTGTCCTGAGAAGGCCACCACCCAGAACGCCAGCCATGAAGGCAGCTACCTGC
TGCAGCCCTGAAGGCCCTGGCCTAGCCTGGAGCCCAGGACC**TAA**GTCCACCTCACCTAGAG
CCTGGAATTAGGATCCCAGAGTTAGCCAGCCTGGGTCCAGAACTCAAGAGTCCGCTGCT
TGGAGCTGGACCCAGCGGCCAGAGTCTAGCCAGCTGGCTCCAATAGGAGCTCAGTGGCC
TAAGGAGATGGCCTGGGTGGGGCTTATGAGTTGGTCTAGAGCCAGGGCCATCTGGACT
ATGCTCCATCCAAGGGCAAGGGTCAGGGCCGGTCCACTCTTCCTAGGCTGAGCACC
TCTAGGCCCTCTAGGTTGGGAAGCAAACGGAACCCATGGCAATAATAGGAGGGTGTCCAG
GCTGGCCCTCCCTGGCCTCCAGTGGATAATAATGGAACATGGCTCTAA
AAAAAAAAAAAAAAA

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FIGURE 109

MGAAISQGALIAIVCNGLVGFL_{LLL}LWVILCWACHSRLPTTLSLN_PVPTPALAPVLRRPHH
PRSPAMKAATCCSPEGPWPSLEPRT

FIGURE 110

GTTTGAATTCTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCA
 GTTCCTCCAAGCAAGTCATTCCTTATTAAACCGATGTGTCCCTCAAACACCTGAGTGCTA
 CTCCCTATTCGATCTGTTGATAATGATGTTGACACCCTCCACCGAATTCTAAGTGGAA
TCATGTCGGGAAAGAGATACAATCCTGGCCTGTATCCTCGCATTAGCCTGTCTTGGCC
 ATGATGTTACCTTCAGATTCATCACCAACCCTCTGGTCACATTTCTTCATTGTTAT
 TTTGGGATTGTTGTTGTCGCGGTGTTATGGTGGCTGTATTATGACTATACCAACGACC
 TCAGCATAGAATTGGACACAGAAAGGGAAAATATGAAGTGCCTGCTGGGTTGCTATCGTA
 TCCACAGGCATCACGGCAGTGCTGCTCGTCTGATTTGTTCTCAGAAAGAGAATAAAATT
 GACAGTTGAGCTTTCCAAATCACAAATAAGCCATCAGCAGTGCTCCCTCCTGCTGTTCC
 AGCCACTGTGGACATTGCCATCCTCATTCTCTGGTCCTCTGGGTGGCTGTGCTGCTG
 AGCCTGGGAACTGCAGGAGCTGCCAGGTTATGGAAGGCGGCCAAGTGAATATAAGCCCT
 TTCGGGCATTGGTACATGTGGTGTACCTTAATTGGCCTCATCTGGACTAGTGAATTCA
 TCCTTGCCTGCCAGCAAATGACTATAGCTGGGCAGTGGTTACTGTATTCACAGAAGT
 AAAAATGATCCTCCTGATCATCCCATTCTCGTCTCTCCATTCTCTTCTACCATCA
 AGGAACCCTGTGAAAGGGTCATTAAATCTCTGTGGTGAGGATTCCGAGAACATTGTCA
 TGTACATGCAAACGCAGTGAAAGAACAGCAGCATGGTGCATTGTCCAGGTACCTGTTCCGA
 TGCTGCTACTGCTGTTCTGGTGTCTGACAAATACCTGCTCCATCTAACCGAGAACATGCATA
 TACTACAACGTCTATTAAATGGGACAGATTCTGTACATCAGCAAAGATGCATTCAAATCT
 TGTCCAAGAACTCAAGTCACCTTACATCTATTAACTGCTTGAGACTTCATAATTCTCTA
 GGAAAGGTGTTAGTGGTGTGTTCACTGTTGGAGGACTCATGGCTTTAACTACAATCG
 GGCATTCCAGGTGTGGCAGTCCCTCTGTTATTGGTAGCTTTGCCTACTTAGTACCC
 ATAGTTTTATCTGTGTTGAAACTGTGCTGGATGCACCTTCCTGTGTTGCTGTTGAT
 CTGGAAACAAATGATGGATCGTCAGAAAAGCCCTACTTATGGATCAAGAACATTCTGAGTT
 CGTAAAAAGGAGCAACAAATTAAACATGCAAGGGCACAGCAGGACAAGCACTCATTAAGGA
 ATGAGGAGGAAACAGAACTCCAGGCCATTGTGAGA**TAG**ATACCCATTAGGTATCTGTACCT
 GGAAAACATTCCTCTAAGAGCCATTACAGAAATAGAAGATGAGACCACTAGAGAAAAGTT
 AGTGAATTTTTTAAAAGACCTAATAAACCTATTCTCCTCAAAA

FIGURE 111

MSGRDTILGLCILALALS LAMMFTFRFITTLLVHIFISLVLG LLVMFVCGV LWL YYD YTN DL
SIEL DTERENMKCVLGFAIVSTGITAVLLVLIFVLRKRIKLTVELFQITNKAIS SAP FLL FQ
PLW TFAILIFFWVLWVAVLLSLGTAGAAQVM EGGQVEYKPLSGIRYMW SYHLIGLIWTSEFI
LACQQMTIAGAVVTCYFNRSKNDPPDHPI LSSLSILFFYHQGTVVKG SFLISVVRIPRI IVM
YMQN ALKEQQHGALSRYLFRC CYYCCFWCLDKYLLHLNQNAYTTAINGTDFCTS AKA DF KIL
SKN S SHFTSINC GDFIIFLGKV LVVCFTVFGGLMAFNYNRAF QVWA VPLLVAFFAYLVAH
SFLSVFETVLDALFLCFAVDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQ QDKHSLRN
EEGTELOQAIVR

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FIGURE 112

GTTCGATTAGCTCCTCTGAGAAGAAGAGAAAAGGTTCTGGACCTCTCCCTGTTCTTCCTT
 AGAATAATTGTATGGGATTGTGATGCAGGAAAGCTAACAGGAAAAGAATATTCAATTCTG
 TGTGGTGAAGAATTTTGAAAAAAATTGCCTCTCAAACAAGGGTGTCAATTCTGATATT
TATGAGGACTGTTCTCACTATGAAGGCATCTGTTATTGAAATGTCCTGTTGCTGG
 TGACTGGAGTACATTCAAACAAAGAACGGCAAAGAAGATTAAAAGGCCAAGTTCACTGTG
 CCTCAGATCAACTGCATGTCAAAGCCGAAAGATCATCGATCCTGAGTTCATGTGAAATG
 TCCAGCAGGATGCCAAGACCCCCAAATACCATGTTATGGCACTGACGTGTATGCATCCTACT
 CCAGTGTGTGGCGTGCCTCACAGTGGTGTGTTGATAATTCAACGGGTGTCATCGTT
 GTTCGGAAGGTTGCTGGAGACTGCTGGTTACAAAGGGAGTTATTCCAACGGGTGTCATCGTT
 ATCCCTACCACAGTGGAGAGAATCCTTATCGTCTAGAAAGTAAACCAAAAAGGGTGTAA
 CCTACCCATCAGCTCTACATACATCATCGAAAAGTCCAGCTGCCAAGCAGGTGAGACC
 ACAAAAGCTATCAGAGGCCACCTATTCCAGGGACAACGTGACAGCCGGTCACTGTGATGCA
 GCTTCTGGCTGTCAGTAGCTGTGGCCACCCCCACACCTGCCAAGGCCATCCCCTCTG
 CTGCTTCTACCACAGCATCCCCAGACCAATCAGTGGGCCACAGGAGCCAGGAGATGGAT
 CTCTGGTCCACTGCCACCTACACAAGCAGCCAAAACAGGCCAGAGCTGATCCAGGTATCCA
 AAGGCAAGATCCTCAGGAGCTGCCTTCAGAAACCTGTTGGAGCGGATGTCAGCCTGGGAC
 TTGTTCAAAGAAGAATTGAGCACACAGTCTTGAGGCCAGTATCCCTGGGAGATCCAAC
 TGCAAATTGACTGTCGTTTAATTGATGGGAGCACAGCATTGGCAAACGGCATTCCG
 AATCCAGAAGCAGCTCCTGGCTGATGTTGCCAAGCTTGTGACATTGCCCTGCCGGTCAC
 TGATGGGTGTTGTCAGTGGAGACAACCCCTGCTACTCATTAACTCAAGACACACAG
 AATTCTCGAGATCTGAAGACAGCCATAGAGAAAATTACTCAGAGAGGAGACTTCTAATGT
 AGGTGGGGCCATCTCCTTGTGACCAAGAACTTCTTCCAAAGCCAATGGAAACAGAACG
 AGGTGGGGCCATCTCCTTGTGACCAAGAACTTCTTCCAAAGCCAATGGAAACAGAACG
 GGGCTCCAATGTGGTGGTGTGGCTGGGAGACTGGCTGGCCACGGACAAAGTGGAGGAGGCT
 TCAAGACTTGCGAGAGAGTCAGGAATCAACATTTCATCACCATTGAAGGTGCTGCTGA
 AAATGAGAAGCAGTATGTGGTGGAGCCAACCTTGCAAACAAGGCCGTGTCAGAACAAACG
 GCTTCTACTCGCTCCACGTGCAGAGCTGGTTGGCCTCCACAGACCTGCAGCCTCTGGT
 AAGCGGGTCTGCGACACTGACCGCCTGGCTGCAGCAAGACACTGCTGAACCTGGCTGACAT
 TGGCTCGTCATCGACGCTCCAGCAGTGTGGGAGCGGGCAACTCCGCACCGTCCTCCAGT
 TTGTTGACCAACCTCACCAAAGAGTTGAGATTCCGACACGGACACCGCATTGGGGCCGTG
 CAGTACACCTACGAACAGCGGCTGGAGTTGGTTGACAAAGTACAGCAGCAAGCCTGACAT
 CCTCAACGCCATCAAGAGGGTGGCTACTGGAGTTGGCAGCAGCACGGGGCTGCCATCA
 ACTTCGCCCTGGAGCAGCTTCAGAACAGTCAACAGGCCAACAAAGAGGAAGTTAATGATCCTC
 ATCACCGACGGGAGGTCTACGACGACGTCGGATCCCAGCCATGGCTGCCCATCTGAAGGG
 AGTGTACACCTATGCGATAGGCCTGGCTGGCTGCCAACAGAGGAGCTAGAAGTCATTGCCA
 CTCACCCGCCAGAGACCACTCCCTCTTGTGGACGAGTTGACAACCTCCATCAGTATGTC
 CCCAGGATCATCCAGAACATTGTACAGAGTTCAACTCACAGCCTCGGAAC**TGA**ATTCAAGAG
 CAGGCAGAGCACCAGCAAGTGTGCTTTACTAAGTGCACGTGTTGGACCAACCCACCGCTTAA
 TGGGGCACGCACGGTGCATCAAGTCTGGCAGGGCATGGAGAAACAAATGTCCTGTTATTA
 TTCTTGTGCATCATGCTTTCATATTCCAAAAGTGGAGTTACAAAGATGATCACAAACGT
 ATAGAATGAGCAAAAGGCTACATCATGTTGAGGGTGTGGAGATTACATTGACAATT
 GTTTCAAAATAATGTCGGAATACAGTGCAGCCCTACGACAGGCTTACGTAGAGCTTT
 GTGAGATTAAAGTTGCTGATTGAACTCTGTAACCCCTCAGCAAGTTCAATT
 GTCATGACAATGAGGAATTGCTGAATTAAATGTTAGAAGGATGAAAAAATAAAAAAA
 AAAG

FIGURE 113

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKC
PAGCQDPKYHVGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNGVQSL
SLPRWRESFIVLESKPKKGVTPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQPVTLMQ
LLAVTVAVATPTTLPRPSAATTSIPRPQSVGHRSQEMDLWSTATYTSSQRPRADPGIQ
RQDPSGAAFQKPGVADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSPFLIDSTSIGKRRFR
IQKQLLADVAQALDIGPAGPLMGVVQYGDNPATHFNLKHTNSRDLKTAIEKITQRGGLSNV
GRAISFVTKNFFSKANGNRSGAPNVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAE
NEKQYVVEPNFANKAVCRTNGFYSLHVQSWFGLHKTLPQPLVKRVCDTDRLACSKTCLNSADI
GFVIDGSSSVGTGNFRTVLQFVTNLTKFEISDTDTRIGAVQTYEQRLEFGFDKYSSKPDI
LNIAIKRVEGYWSGGTSTGAAINFALQLFKKS KPNKRKLMILITDGRSYDDVRI PAMAAHLKG
VITYAIGVAWAQEELEVIATHPARDHSFFVDEFDNLHQYVPRITQNICTEFNSQPRN

FIGURE 114

CAGGATGAACGGTTGCAGTGGCTGCTGCTGCCGGGGCGCTGAGAGGACACGAGCTCTA
TGCCTTCGGCTGCTCATCCGCTCGGCCTCCTGTGCGCCTGCTGCCTCAGCACCATGGT
 GCGCCAGGTCCCGACGGCTCCGCCAGATCCGCCACTACAGTTTCTGACTCTAAT
 TGATGCACTGGACACCTTGCTGATTGGAAATGTCTCAGAATTCAAAGAGTGGTTGAAG
 TGCTCCAGGACAGCGTGGACTTGATATTGATGTGAACGCCTCTGTGTTGAAACAAACATT
 CGAGTGGTAGGAGGACTCCTGTCTGCTCATCTGCTCTCCAAGAAGGCTGGGTGGAAGTAGA
 GGCTGGATGGCCCTGTTCCGGGCCTCCTGAGAATGGCTGAGGAGGCCGCCCCAAAACCTCC
 TCCCAGCCTTCAGACCCCCACTGGCATGCCATATGGAACAGTGAACTTACTCATGGCGTG
 AACCCAGGAGAGACCCCTGTCACCTGTACGGCAGGGATTGGGACCTTCATTGTTGAATTG
 CACCCCTGAGCAGCCTCACTGGTACCCGGTGTCAAGATGTGGCCAGAGTGGCTTGATGC
 GCCTCTGGGAGAGCCGGTCAGATATCGGGCTGGTGGCAACCACATTGATGTGCTCACTGGC
 AAGTGGGTGGCCCAAGGACGCAGGCATGGGGCTGGGTGGACTCCTACTTGAGTACTGGT
 GAAAGGAGCCATCCTGTTCAAGGATAAGAACGCTCATGGCATGTTCTAGAGTATAACAAAG
 CCATCCGGAACTACACCCGCTTCGATGACTGGTACCTGTGGGTTCAAGATGTACAAGGGACT
 GTGTCCATGCCAGTCTTCAGTCCTGGAGGCCTACTGGCCTGGTCTCAGAGCCTCATGG
 AGACATTGACAATGCCATGAGGACCTTCCTCAACTACTACACTGTATGGAAGCAGTTGGG
 GGCTCCGGAATTCTACAACATTCTCAGGGATAACAGTGGAGAAGCGAGAGGGCTACCCA
 CTTCGCCAGAACTTATTGAAAGCGCAATGTACCTCTACCGTGCACGGGGATCCCACCC
 CCTAGAAACTCGGAAGAGATGCTGTGGAATCCATTGAAAAAAATCAGCAAGGTGGAGTGC
 TTGCAACAATCAAAGATCTGCGAGACCACAAGCTGGACAACCGCATGGAGTCGTTCTC
 GCCGAGACTGTGAAATACTCTACCTCTACCTGTTGACCCACCAACTCATCCACAACATGG
 GTCCACCTCGACCGGTGATCACCCCTATGGGAGTGCATCCTGGGGCTGGGGTACA
 TCTTCAACACAGAACGCTCACCCATGACCTGGCCCTGCACGTGCTGCCAGAGGCTGAAG
 GAAGAGCAGTGGGAGGTGGAGGACTTGATGAGGAATTCTACTCTCAAACGGAGCAGGTC
 GAAATTCAAGAAAACACTGTTAGTCGGGCCATGGAACCTCCAGCAAGGCCAGGAACAC
 TCTTCTCACCAGAAAACCATGACCAGGCAAGGGAGAGGAAGCCTGCCAACAGAAGGT
 CTTCTCAGCTGCCCAAGTCAGCCCTCACCTCAAGTTGGCATTACTGGGACAGGTTTC
 AGACTCCTCATAACCACTGGATAATTTTTATTTTTATTGGAGGCTAAACTATAATA
 ATTGCTTTGGCTATCATAAAA

FIGURE 115

MPFRLLIPLGLL CALL PQHHGAPGP DGSAPDPAHYSFS LTLIDALDTLLILGNVSE FQRVVE
VLQDSVDFDIDVN ASVFETNIRVVGGLLSAHLLSKKAGVEVEAGWPCSGPLL RMAEEAARKL
LPAFQTPTGMPYGT VNLLHG VNPGETPVTCTAG IGT FIVEFATISSL TGDPV FEDVARVALM
RLWESRSDIGLVGNHIDVLTGKWVAQDAGIGAGVDSYFEYLVKGAILLQDKKL MAMFLEYNK
AIRNYTRFDDWYLWVQMYKGTVSMPVFQSLEAYWPGLQSLIGDIDNAMRTFLNYYTVWKQFG
GLPEFYNI PQGYTVEKREGYPLR PELIESAMYLYRATGDPTLLELGRDAVESIEKISKVECG
FATIKDLRDHKLDNRMESFFLAETVKYLYLLFDPTNFIHNGSTFDAVITPYGECILGAGGY
IFNTEAHPIDLAALHCCQRLKEEQWEVEDILMREFYSLKRSRSKFQKNTVSSGPWEPPARPGT
LFSPENHDQARERKPAKQKVPLLSCPSQPFTSKLALLGQVFLDSS

FIGURE 116

AAAGTTACATTTCTCTGGAACCTCCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG
 GGCAGAAAGGAGGGTGCTCGGAGCCCGCCCTTCTGAGCTCCTGGGCCGGCTAGAACAA
 ATTCAGGCTTCGCTGCGACTCAGACCTCAGCTCAAACATATGCATTCTGAAGAAAGATGGCT
 GAGATGGACAGAATGCTTATTTGAAAGAACAAATGTTCTAGGTCAAACAGTACCA
AATGCAGACTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTCATGTGGTTTTCT
 ACGCATTGATTCCATGTTGCTCACAGATGAAGTGGCCATTCTGCCTGCCCTCAGAACCTC
 TCTGTACTCTCAACCAACATGAAGCATCTTGATGTGGAGCCCAGTGATCGCGCTGGAGA
 AACAGTGTACTATTCTGTCGAATACCAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCT
 GGATCCCCAGCAGCTGGTGCCTACTCACTGAAGGTCTGAGTGTGATGTCAGTGACATC
 ACGGCCACTGTGCCATACAACCTTCGTGTCAGGGCCACATTGGCTCACAGACCTCAGCCTG
 GAGCATCCTGAAGCATCCCTTAATAGAAACTCAACCACCTTACCCGACCTGGGATGGAGA
 TCACCAAAGATGGCTTCCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCAAGTTGAGTTC
 CTTGTGGCCTACTGGAGGGAGCCTGGTGCCGAGGAACATGTCAAAATGGTGAGGAGTGG
 GGGTATTCCAGTGCACCTAGAAACCATGGAGCCAGGGCTGCATACTGTGAAAGGCCAGA
 CATTGTAAGGCCATTGGAGGTACAGCGCCTTCAGCCAGACAGAACATGTGGAGGTGCAA
 GGAGAGGCCATTCCCTGGTACTGGCCCTGTTGCCTTGTGGCTTATGCTGATCCTGT
 GGCGTGCCTACTGTTGTCCTGGAAAATGGGCCGGCTGCTCCAGTACTCCTGTTGCCCGTGG
 TGGTCCTCCCAGACACCTTGAAAATAACCAATTCAACCCAGAAGTTAACAGCTGAGAAGG
 GAGGAGGTGGATGCCTGTGCCACGGCTGTGATGTCCTGAGGAACCTCCTCAGGGCCTGGAT
 CTCATAGTTGCGGAAGGGCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAAACC
 ATGAGGGACAAGTTGTTCTGTTCCGCCACGGACAAGGGATGAGAGAAAGTAGGAAGA
 GCCTGTTGCTACAAGTCTAGAACGCAACCACAGAGGCAGGGTGGTTGTCTAACAGAACAC
 TGACTGAGGCTAGGGATGTGACCTCTAGACTGGGGCTGCCACTTGCTGGCTGAGCAACC
 CTGGAAAAGTGACTTCATCCCTCGGTCTAAAGTTCTCATCTGTAATGGGAAATTACC
 TACACACCTGCTAACACACACACAGAGTCTCTCTATATACACACGTACACATAAA
 TACACCCAGCAGTGCAGGCTAGAGGGAAACTGGTGACACTCTACAGTCTGACTGATTGAG
 TGTTCTGGAGAGCAGGACATAATGTATGAGAATGATCAAGGACTCTACACACTGGGT
 GGCTTGGAGAGGCCACTTCCCAGAATAATCCTGAGAGAAAAGGAATCATGGAGCAATGG
 TGTTGAGTTCACTCAAGCCAATGCCGGTGCAGAGGGGAATGGCTAGCGAGCTACAGT
 AGGTGACCTGGAGGAAGGTACAGCCACACTGAAAATGGGATGTGCATGAACACGGAGGATC
 CATGAACACTGTAAAGTGTGACAGTGTGACACTGCAGACAGCAGGTGAAATGTATGT
 GTGCAATGCGACGAGAATGCAGAACAGTCAGTAACATGTGCATGTTGTCCTTTTC
 TGTTGGTAAAGTACAGAATTCAAGCAAATAAAAGGGCCACCCTGGCCAAAAGCGGTAAAAAA
 AAAAAAAA

FIGURE 117

MQTFTMVLEEIWTSLFMWFFYALIPCLLTDEVAILPAPQNLSQLSTNMKHLLMWSPVIAPGE
TVYYSVHEYQGEYESLYTSHIWIPSSWCSLTERGPECVTDDITATVPYNLRVRATLGSQTSAW
SILKHPFNRNSTILTRPGMEITKDGFLVIELEDLGPQFEFLVAYWRREPGAEHHVKMVRSG
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIPLVLALFAFGFMLILV
VVPLFWKMGRLLQYSCCPVVLPDTLKINTSPQKLISCRREVDACATAVMSPEELLRAWIS

Important features:

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 230-255

N-glycosylation sites.

amino acids 40-43 and 134-137

Tissue factor proteins homology.

amino acids 92-119

Integrins alpha chain protein homology.

amino acids 232-262

FIGURE 118

TCTCTGATGCACATCTGGTTGGCAAAAGGAGGTTGCTCGAGCCGCCCTTAGCTT
CCTGGCCGGCTCTAGAACATTAGGCTCGACTAGACCTCAGCTCCAACATATGCA
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTATTTGGAAAGAAACAATGTTCTAGG
TCAAACGTGACTACCAAATGCAGACTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT
TTTCATGTGGTTTCTACGCATTGATTCCATGTTGCTCACAGATGAAGTGCCATTCTGC
CTGCCCTCAGAACCTCTGTACTCTAACCAACATGAAGCATCTTGTGGAGGCCA
GTGATCGCGCCTGGAGAACAGTGTACTATTCTGTGAATACCAGGGGAGTACGAGAGCCT
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGTCACTCACTGAAGGTCTGAGTGTG
ATGTCAGTGTGACATCACGCCACTGTGCCATACAACCTTGTGTCAAGGCCACATTGGGC
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTAATAGAAACTCAACCACCTTAC
CCGACCTGGATGGAGATCACCAAAGATGGCTNCACCTGGTTATTGAGCTGGAGGACCTGG
GGCCCCAGTTGAGTCTCTGTGGCCTANTGGAGGGCGAACCCCTTGCGCGCAAGGG
GTTNGCGAACCCCTTGCGGCCGCTGGGTATCTCTCGAGAAAAGAGAGGCCAATATGACCCAC
ATACTCAATATGGACGAANTGCTATTGTCCACCTGTTGAGTGGCGCTGGTTGAT

FIGURE 119

CGGACGCGTGGGCCACCTCCGAACAAGCC**ATG**GTGGCGCGACGGTGGCAGCGCGTG
 GCTGCTCTGTGGCTGC GGCTGCGCGCAGCAGGAGCAGGACTTCTACGACTTCAGCAAGGCGG
 TCAACATCCGGGGCAAACCTGGTGTGCGCTGGAGAAGTACCGCGGATCGGTGTCCCTGGTGGTG
 AATGTGGCCAGCGAGTGC GGCTCACAGACCAGCACTACCGAGCCCTGCAGCAGCTGCAGCG
 AGACCTGGGCCCCCACCACTTAACGTGCTGCCTCCCCTGCAACCAGTTGGCCAACAGG
 AGCCTGACAGCAACAAGGAGATTGAGAGCTTGCCCGCACCTACAGTGTCTCATTCCCC
 ATGTTAGCAAGATTGCAGTCACCGTACTGGTGCCCATCCTGCCTCAAGTACCTGGCCA
 GACTTCTGGGAAGGAGCCCACCTGGAACCTCTGGAAGTACCTAGTAGCCCCAGATGGAAAGG
 TGGTAGGGCTGGGACCCAACTGTGTCA GTGGAGGAGGT CAGACCCAGATCACAGCGCTC
 GTGAGGAAGCTCATCCTACTGAAGCGAGAACACTTA**TAA**CCACCGCGTCTCCTCCTCCACCA
 CCTCATCCGCCACCTGTGTGGGCTGACCAATGCAAACCTCAAATGGTGCTCAAAGGGAG
 AGACCCACTGACTCTCCTCCTTACTCTTATGCCATTGGTCCCATCATTCTGTGGGGAA
 AAATTCTAGTATTTGATTATTGAATCTTACAGCAACAAATAGGAACCTCTGGCAATGAG
 AGCTCTGACCAGTGAATCACCAAGCCGATACGAACGTCTGCCAACAAAATGTGTGGCAA
 TAGAAGTATATCAAGCAATAATCTCCACCCAAAGGCTCTGTAAACTGGGACCAATGATTAC
 CTCATAGGGCTGTTGTGAGGATTAGGATGAAATACCTGTGAAAGTGCCTAGGCAGTGCCAGC
 CAAATAGGAGGCATTCAATGAACATTTTGATATAAACAAAAAAACTTGTATCAAT
 AAAAACTTGCATCCAACATGAATTCCAGCCGATGATAATCCAGGCCAAAGGTTAGTTGTT
 GTTATTCCTCTGTATTATTTCTTCATTACAAAAGAAATGCAAGTTATTGTAACAATCCA
 AACAAACCTCACGATATAAAATGAAAGTATCCTCCTCAAAA

FIGURE 120

MVAATVAAWLLLWAAACAQQEQDFYDFKAVNIRGKLVSLKYRGSVSLVVNVASECGFTDQ
HYRALQLQRDLGPHHFNVLAFTPNCNQFGQQEPDSNKEIESFARRTYSVSFPMFSKIAVTGTG
AHPAFKYLAQTSGKEPTWNFWKYLVAPDGKVVGAWDPTVSVEVRPQITALVRKLILLKREDL

FIGURE 121

CGGACGCCTGGCGGGCCGGGACGCAGGGCAAAGCGAGCC**ATG**GCTGTCTACGTGGGATGC
 TCGCCTGGGAGGCTGTGCGCCGGGAGCTCGGGGGTGTGGGGGCCGGGCCCTCTCT
 CGGAGTTGGCAGGAAGCCAGGTTGCAGGGTGTCCGCTTCCTCAGTTCCAGAGAGGTGGATCG
 CATGGTCTCCACGCCATCGGAGGCCTCAGCTACGTTCAGGGGTGCACCAAAAGCATCTTA
 ACAGCAAGACTGTGGGCCAGTGCCTGGAGACCACAGCACAGAGGGTCCCAGAACGAGAGGCC
 TTGGTCGTCTCCATGAAGACGTAGGTTGACCTTGCCCAACTCAAGGAGGAGGTGGACAA
 AGCTGCTTCTGGCCTCCTGAGCATTGGCCTCTGCAAAGGTGACCGGCTGGGATGTGGGAC
 CTAACTCCTATGCATGGGTGCTCATGCAGTTGCCACCGGCCAGGGCATCATTCTGGTG
 TCTGTGAACCCAGCCTACCAGGCTATGAACTGGAGTATGTCCTCAAGAAGGTGGCTGCAA
 GGCCCTTGTGTTCCCCAAGCAATTCAAGACCCAGCAATACTACAACGTCTGAAGCAGATCT
 GTCCAGAAGTGGAGAATGCCAGCCAGGGCCTTGAAGAGTCAGAGGCTCCAGATCTGACC
 ACAGTCATCTCGGTGGATGCCCTTGCAGGGGACCCCTGCTCCTGGATGAAGTGGTGGCGC
 TGGCAGCACACGGCAGCATCTGGACCAGCTCCAATACAACCAGCAGTCCCTGTCCTGCCATG
 ACCCCATCAACATCCAGTTCACCTGGGGACAACAGGCAGCCCCAACGGGGCACCCCTCTCC
 CACTACAACATTGTCACAAACTCCAACATTCTAGGAGAGCCTGAAACTGCATGAGAAC
 ACCAGAGCAGTTGGGATGATCCTGCCAACCCCTGTACCTATTGCCTGGGTTCCGTGGCAG
 GCACAAATGATGTTGATGTACGGTGCACCCCTCATCCTGGCCTCTCCATCTCAATGGC
 AAGAAGGCAGTGGAGGCCATCAGCAGAGAGAGAGGACCTTCTGTATGGTACCCCCACGAT
 GTTCGTGGACATTCTGAACCAGCCAGACTCTCCAGTTATGACATCTCGACCATGTGTGGAG
 GTGTCAATTGCTGGTCCCTGCACCTCCAGGTTGATCCGAGGCATCATCAACAAAGATAAAAT
 ATGAAGGACCTGGTGGTTGCTTATGGAACACAGAGAACAGTCCGTGACATTGCGCAGTT
 CCCTGAGGACACTGTGGAGCAGAAGGCAGAAAGCGTGGCAGAATTATGCCACACGGAGG
 CCCGGATCATGAACATGGAGGCAGGGACGCTGGCAAAGCTGAACACGCCGGGAGCTGTGC
 ATCCGAGGGTACTGCGTCATGCTGGCTACTGGGTGAGCCTCAGAACAGAGAGAAC
 GGATCAGGACAAGTGGTATTGGACAGGAGATGTCGCCACAATGAATGAGCAGGGCTTCTGCA
 AGATCGTGGCCGCTAAGGATATGATCATCCGGGTGGTGAGAACATCTACCCCGCAGAG
 CTCGAGGACTCTTACACACACCCGAAGGTGCAGGAAGTGCAGGTGGTGGAGTGAAGGA
 CGATCGGATGGGGAAGAGATTGTGCCTGCATTGGCTGAAGGACGGGAGGAGAACACGG
 TGGAGGAGATAAAAGCTTCTGCAAAGGGAAGATCTCTCACCTCAAGATTCCGAAGTACATC
 GTGTTGTCACAAACTACCCCTCACCATTCAAGGAAAGATCCAGAAATTCAAACCTCGAGA
 GCAGATGGAACGACATCTAAATCTG**TGA**ATAAAAGCAGCAGGCCCTGCTGGCCGGTTGGCTT
 GACTCTCTCTGTCAGAATGCAACCTGGCTTATGCACCTAGATGTCCCCAGCACCCAGTTC
 TGAGCCAGGCACATCAAATGTCAAGGAATTGACTGAACGAACAAAGAGCTCCTGGATGGTC
 CGGGAACTCGCTGGCACAAGGTGCCAAAGGCAGGCAGCCTGCCAGGCCCTCCCTCCTG
 TCCATCCCCACATTCCCTGTCCTGTGATTGGCATAAAGAGCTTGTGTTTCTT
 GAAAAAAA

FIGURE 122

MAVYVGMLRLGRLCAGSSGVLGARAALSRSWQEARLQGVRFLLSREVDRMVSTPIGGLSYVQ
GCTKKHLNSKTVQCLETTAQRVPEREALVVLHEDVRLTFAQLKEEVDKAASGLLSIGLCKG
DRLGMWGPNSYAWVLMQLATAQAGIILVSVNPAYQAMELEYVLKKVGCKALVFPKQFKTQQY
YNVLKQICPEVENAQPGALKSQRLPDLTVISVDAPLPGTLLLDEVVAAGSTRQHLDQLQYN
QQFLSCHDPINIQFTSGTGSPKGATLSHYNIVNNNSNILERLKLHEKTPEQLRMILPNPLY
HCLGSVAGTMMCLMYGATLILASPIFNGKKALEAISRERGTFLYGTPTMFVDILNQPDFSSY
DISTMCGGVIAGSPAPPELIRAIINKINMKDLVVAYGTTENSPVTFAHFPEDTVEQKAESVG
RIMPHTEARIMNMEAGTLAKLNTPGELCIRGYCVMLGYWGEPKTEEAVDQDKWYWTGDVAT
MNEQGFCKIVGRSKDMIIRGGENIYPAELEDFFHHPKVQEJVQVVGVKDDRMGEEICACIRL
KDGEETTVEEIKAFCKKGKISHFKIPKYIVFVTNYPLTISGKIQKFKLREQMERHLNL

Signal Peptide:

amino acids 1-22

Transmembrane Domains:

amino acids 140-161, 213-229, 312-334

Putative AMP-binding Domain Signature:

amino acids 260-271

N-myristoylation Sites:

amino acids 19-24, 22-27, 120-125, 203-208, 268-273, 272-277,
314-319, 318-323, 379-384, 380-385, 409-413

N-glycosylation Site:

amino acids 282-285

FIGURE 123

CAACTCCAACATTTAGGAGAGCGCCTGAAACTGCATGAGAAGACACCAGAGCAGTTGCGGA
TGATCCTGCCAACCCCTGTACCATTGCCTGGGTTCCGTGGCAGGCACAATGATGTGTCTG
ATGTACGGTGCCACCCCTCATCCTGGCCTCTCCATCTTCATGGCAAGAAGGCACGGAGGC
CATCAGCAGAGAGAGAGGACACCTCCTGTATGGTACCCCCACGATGTTCGTGGACATTCTGA
ACCAGCCAGACTTCTCCAGTTATGACATCTGACCATGTGTGGAGGTGTCATTGCTGGTCC
CCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAAATATGAAGGACCTGGTGGT
TGCTTATGGAACCACAGAGAACAGTCCCGTGCACATTGCGCACCTCCCTGAGGACACTGTGG
AGCAGAAGGCAGAAAGCGTGGCAGAATTATGCCTCACACGGAGGCGCGGATCATGAACATG
GAGGCAGGGACGCTGGCAAAGCTGAACACGCCCGGGAGCTGTGCATCCGAGGGTACTGCGT
CATGCTGGCTACTGGGTGAGCCTCAGAAGACAGAGGAAGCAGTGGATCAGGACAAGTGGT
ATTGGACAGGAGATGTCGCCAC

FIGURE 124

GAGCAGGACGGAGCCATGGACCCGCCAGAAAGCAGGTGCCAGGCCATGATCTGGACTGC
 AGGCTGGCTGCTGCTGCTGCTCGCGGAGGAGCGCAGGCCCTGGAGTGCTACAGCTGCG
 TGCAGAAAGCAGATGACGGATGCTCCCCGAACAAGATGAAGACAGTGAAGTGCGCGCCGGC
 GTGGACGTCTGCACCGAGGCCGTGGGGCGGTGGAGACCATCCACGGACAATTCTGCTGGC
 AGTGCGGGTTGCGGTTGGACTCCCCGGCAAGAATGACCGCGGCCTGGATCTCACGGGC
 TTCTGGCGTTCATCCAGCTGCAGCAATGCCTCAGGATCGCTGCAACGCCAAGCTAACCTC
 ACCTCGCGGGCGCTCGACCCGGCAGGTAAATGAGAGTGCATAACCGCCAACGGCGTGGAGTG
 CTACAGCTGTGTGGCCTGAGCCGGAGGCCTGCCAGGGTACATGCCGCCGGTGTGAGCT
 GCTACAACGCCAGCGATCATGTCTACAAGGGCTGCTCGACGGCAACGTCACCTGACGGCA
 GCTAATGTGACTGTGTCCCTGCCTGTCCGGGCTGTGTCCAGGATGAATTCTGCACTCGGGA
 TGGAGTAACAGGCCAGGGTTCACGCTCAGTGGCTCTGTTGCCAGGGTCCCGCTGTAAC
 CTGACCTCCGCAACAAGACCTACTTCTCCCTCGAATCCCACCCCTTGTCCGGCTGCCCT
 CCAGAGCCCACGACTGTGGCCTAACCACATCTGTCACCACCTACCTCGGCCAGTGAG
 ACCCACATCCACCACCAAACCCATGCCAGGCCAACAGTCAGACTCCGAGACAGGGAGTAG
 AACACGAGGCCTCCCGGGATGAGGAGGCCAGGTTGACTGGAGGCCGCTGGCCACCAGGAC
 CGCAGCAATTCAAGGCAGTATCCTGCAAAAGGGGGCCCGAGCAGCCCCATAATAAAGGCTG
 TGTGGCTCCCACAGCTGGATTGGCAGCCCTCTGTTGCCGTGGCTGCTGGTGTCTACTGTT
GAGCTTCTCCACCTGGAAATTCCCTCTCACCTACTTCTCTGCCCTGGTACCCCTTTCT
 CATCACTTCCCTGTTCCCACCACTGGACTGGCTGGCCAGCCCCTGTTTCCAACATTCCC
 CAGTATCCCCAGCTTCTGCTGCGCTGGTTGCGGCTTGGAAATAAAATACCGTTGTATAT
 ATTCTGCCAGGGTGTCTAGCTTTGAGGACAGCTCTGTATCCTCTCATCCTGTCTC
 TCCGCTTGTCTTGTGATGTTAGGACAGAGTGAGAGAAGTCAGCTGTACGGGAAGGTG
 AGAGAGAGGATGCTAAGCTTCACTCACTTCTCTAGCCAGCCTGGACTTGGAGCGTGG
 GGTGGGTGGACAATGGCTCCCCACTCTAACGACTGCCTCCCTACTCCCCGCATTTGG
 GAATCGGTTCCCCATATGTCTCCTACTAGACTGTGAGCTCCTCGAGGGGGGCCGGTAC
 CCAATTGCCCTATAGTGAGTCGTA

FIGURE 125

MDPARKAGAQAMIWTAGWLLLLLRLGGAQALECYSCVQKADDGCSPNKMKTVKCAPGVDVCT
EAVGAVETIHGQFSLAVRGCGSGLPGKNDRGLDLHGLLAFIQLQQCAQDRCNAKLNLTSRAL
DPAGNESAYPPNGVECYSCVGLSREACQGTSPPVSCYNASDHVYKGCFDGNVTLTAANVTV
SLPVRCVQDEFCTRDTGVTGPGFTLSGSQCQGSRCNSDLRNKYFSPRIPLVRLPPPEPTT
VASTTSVTTSTSAPVRPTSTTKPMPAPTSQTPRQGVHEASRDEEPRLTGGAAGHQDRSNSG
QYPAKGGPQQPHNKGCVAPTAGLAALLLAVAAGVLL

FIGURE 126

CGGGACTCGGCGGGTCCTCCTGGGAGTCTCGGAGGGGACCGGCCTGTGCAGACGCC**ATGG**GAGT
 TGGTGCTGGTCTCCTCTGCAGCCTGCTGGCCCCATGGTCCTGCCAGTGCAGCTGAAAAG
 GAGAAGGAAATGGACCCTTTCAATTATGATTACCAAGACCCCTGAGGATTGGGGACTGGTGT
 CGCTGTGGTCCTCTCGGTTGGGATCCTCCTTATCCTAACGTCGAGGTGCAAGTGCAGTT
 TCAATCAGAACGCCCCGGGCCCCAGGAGATGAGGAAGGCCAGGTGGAGAACCTCATCACCGCC
 AATGCAACAGAGCCCCAGAACAGAGAACACTGAAGTGCAGCCATCAGGTGGAAGCCTCTGGAA
 CCTGAGGCAGCTGCTTAACCTTGGATGCAAATGTCGATGCT**TAA**AAAACCGGCCACTTC
 AGCAACAGCCCTTCCCCAGGAGAACGCAAGAACACTGTGTGTCCCCACCCCTATCCCCTCTA
 ACACCATTCCACCTGATGATGCAACTAACACTTGCTCTCCACTGCAGCCTGCGGTCT
 GCCCACCTCCCGTATGTGTGTGTGTGTGTACTGTGTGTGTTGCTAACTGTG
 GTCTTGTGGCTACTTGTGTGGATGGTATTGTGTTGTTAGTGAACGTGGACTCGCTT
 CCCAGGCAGGGCTGAGCCACATGCCATCTGCTCTCCGTGCCCTCCATCAC
 CTTCTGCTCCTAGGAGGCTGCTTGTGCCGAGACCAGCCCCCTCCCTGATTAGGGATGC
 GTAGGGTAAGAGCACGGCAGTGGCTTCAGCGTCTGGACCTGGGAAGGTTGCAGCAC
 TTTGTCATCATTCTCATGGACTCCTTCACTCCTTAACAAAAACCTTGCTTCTTATCCC
 ACCTGATCCCAGTCTGAAGGTCTTAGCAACTGGAGATAACAGCAAGGAGCTGGTAGCC
 CAGCGTTGACGTCAAGGCAGGCTATGCCCTCCGTGTTAATTCTCCAGGGCTCCACG
 AGGAGTCCCCATCTGCCCGCCCCCTCACAGAGCGCCGGGATTCCAGGCCAGGGCTTCT
 ACTCTGCCCTGGGAATGTGTCCCCTGCATATCTCTCAGCAATAACTCCATGGCTCTGG
 GACCCTACCCCTCCAACCTTCCCTGCTCTGAGACTCAATCTACAGCCAGCTCATCCAG
 ATGCAGACTACAGTCCCTGCAATTGGGTCTCTGGCAGGCAATAGTTGAAGGACTCCTGTTCC
 GTTGGGCCAGCACACCGGATGGATGGAGGGAGAGCAGAGGCCTTGCTCTGCCTACG
 TCCCCTTAGATGGCAGCAGAGGCAACTCCCGCATCCTTGCTCTGCCTGCGGTGGTCAGA
 GCGGTGAGCGAGGTGGGTTGGAGACTCAGCAGGCTCCGTGCAGCCCTGGAACAGTGAGAG
 GTTGAAGGTATAACGAGAGTGGAACTCAACCCAGATCCGCCCTCCTGCTCTGTGTT
 CCCGCGAAACCAACCAAACCGTGCCTGTGACCCATTGCTGTTCTGTATCGTATCT
 CCTCAACAACAACAGAAAAAGGAATAAAATCCTTGTTCCT

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FIGURE 127

MELVLVFLCSLLAPMVLASAAEKEKEMDPFH^YQTLRIGGLVFAVVLFSVGILLIILSRCK
CSFNQKPRAPGDEEAQVENLITANATEPQKQRTEVQPSGGSLWNLRRLLEPLDANVDA

FIGURE 128

AAACTTGACGCCATGAAGATCCC GGTC TTCCCTGCCGTGGT GCTCCTCTCCCTCCTGGTGCT
CCACTCTGCCAGGGAGCCACCCTGGGTGGTCCTGAGGAAGAAAGCACCATTGAGAATTATG
CGTCACGACCCGAGGCCTTAACACCCCCGTTCTGAACATCGACAAATTGCGATCTGCCTT
AAGGCTGATGAGTT CCTGA ACTGGCACGCCCTTTGAGTCTATCAAAAGGAAACTTCCTT
CCTCAACTGGGATGCCTT CCTAAGCTGAAAGGACTGAGGAGCGCAACTCCTGATGCCAGT
GACCATGACCTCCACTGGAAGAGGGGGCTAGCGTGAGCGCTGATTCTAACCTACCATAACT
CTTCCTGCCTCAGGAACTCCAATAAACATTTCCATCCAAA

FIGURE 129

MKIPVLPAVVLLSLLVLHSAQGATLGGPEEESTIENYASRPEAFNTPFLNIDKLRSAFKADEFLNWHALFESIKRKLPFLNWDAFPKLKGLRSATPDAQ

FIGURE 130

CAGTTCTGAAATCAATGGAGTTAATTAGGAAATACAAACCAGCC**ATG**GGGGTGGAGATTGC
CTTGCGCTCAGTGATTCTCACCTGCCTCTCCCTTCTGGCAGCAGGAGTCTCCCAGGTTGTTCT
TTCTCCAGCCAGTTCCAACTCAGGAGACAGGTCCCAGGCCATGGGAGATCTCTCCTGTGGCT
TTGCCGGCCACTCA**TGA**GAGTGTTTGTGTAAAGTATTTTAGAATACTGTTGACTTCT
TCATGATTAATAACCATCCTTGCAGTAAAGTATGAGGCTTAGGGGAATGTCAACCCTCA
AATTTTGTATACTAGATGGCTTCATTACCCACCACTATTTAAGGTCCCTTATTTT
AGGTTCAAGGTTCATTTGACTTGAGAAAGTGCCTCTGCAGCTCATTGATTGTTATC
TTCACTATTAATTGTAACGATTAAAAAGAATAAGAGCACGCCAGACCTCTAGGAGAATATTT
TATCCCTGGGTGCCCTGACACATTATGTAGTGATCCCACAAATGTGATTGTTAATTTAAA
TGTTATTCTAATATTAGTACATTCAAGTTGTGATGTAATATGAATAACCAGAACATCTATTTCTT
AAAAGTTTGAGTATATTTCAACTAGATATTTGTATAGAAAGACTGAATAGTGATG

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FIGURE 131

MGVEIAFASVILTCLSLLAAGVSQVVLLQPVPTQETGPKAMGDLSCGFAGHS

FIGURE 132

GGGGAATCTGCAGTAGGTCTGCCGCG**ATG**GAGTGGTGGCTAGCTGCCGCTCGGCTCTG
 GCTGCTGTTCTCCTGCCCTAGCGCAGGGCCGCCAGAAGGGAGTCAGGTTCAAATGGA
 AAGTATTATTGACCAAATTAACAGGTCTTGGAGAATTACGAACCATGTTCAAGTCAAAC
 TGCAGCTGCTACCATGGTGTATAGAACAGGATCTAACTCCTTCCGAGGAGGCATCTCCAG
 GAAGATGATGGCAGAGGTAGTCAGACGGAAGCTAGGGACCCACTATCAGATCACTAAGAAC
 GACTGTACCGGGAAAATGACTGCATGTTCCCCTCAAGGTGTAGTGGTGTGAGCAGCTTATT
 TTGGAAGTGATCGGGCGTCTCCCTGACATGGAGATGGTGTCAATGTACGAGATTATCCTCA
 GGTTCCCTAAATGGATGGAGCCTGCCATCCCAGTCTTCCTTCAGTAAGACATCAGAGTACC
 ATGATATCATGTATCCTGCTTGGACATTTGGAAAGGGGGACCTGCTGTTGGCCAATTAT
 CCTACAGGTCTTGGACGGTGGGACCTCTTCAGAGAACATCTGGTAAGGTCAGCAGCACAGTG
 GCCATGGAAAAAGAAAAACTCTACAGCATATTCAGGAGTCAGGACAAGTCCAGAACGAG
 ATCCTCTCATTCTCTGTCTCGGAAAAACCCAAAACCTGTTGATGCGAGAACACACCAAAAC
 CAGGCCTGGAAATCTATGAAAGATACTTAGGAAAGCCAGCTGCTAAGGATGTCCATCTTGT
 GGATCACTGCAAATACAAGTATCTGTTAATTCGAGGCGTAGCTGCAAGTTCCGGTTA
 AACACCTCTCCTGTGGCTCACTGTTTCCATGTTGGTGTAGCTGAGTGGCTAGAATTCTTC
 TATCCACAGCTGAAGCCATGGGTTCACTATATCCCAGTCAAAACAGATCTCTCCAATGTCCA
 AGAGCTGTTACAATTGAAAAGCAAATGATGATGTAGCTCAAGAGATTGCTGAAAGGGAA
 GCCAGTTATTAGGAACCATTGAGATGGATGACATCACCTGTTACTGGGAGAACCTTGTG
 AGTGAATACTCTAAATTCTGTCTTATAATGTAACGAGAACAGGTTATGATCAAATTAT
 TCCCAAAATGTTGAAAAGTGAAC**TAG**TAGTCATCATAGGACCATAGTCCTTTGTGGCA
 ACAGATCTCAGATATCCTACGGTGAGAACGCTTACCATAGCTGGCTCCTACCTTGAAATA
 TCTGCTATCAAGCCAAATACCTGGTTTCTTATCATGCTGCACCCAGAGCAACTCTTGAGA
 AAGATTAAAATGTGTTAAATACACTGATGATGAAGCAGTTCAACTTTGGATGAATAAGGA
 CCAGAAATCGTGGAGATGTGGATTGAAACCCAACTCTACCTTCACTGGTAAATTGACTGTG
 TGTGATGATGCCCTTGTCCCATTATTGGAGCAGAAAATTGTCATTGGAAGTAGTACAA
 CTCATTGCTGGAATTGTGAAATTATTCAAGGCGTGATCTGTCACTTATTTAATGTAGG
 AAACCCATTGGGTTTATGAAAATCTGGGATCATTCTCTGAATGGCTAAGGAAGCGG
 TAGCCATGCCATGCAATGATGTAGGAGTTCTTTGTTAAAACCATAAAACTCTGTTACTCAG
 GAGGTTCTATAATGCCACATAGAAAGAGGCCATTGTCATGAGTAATTATTGCAATTGGATT
 TCAGGTTCCCTTTGTGCCTCATGCCCTACTTCTTAATGCCCTCTAAAGCCAAA

FIGURE 133

MEWWASSPLRLWLLLFLPSAQGRQKESGSWKVFIDQINRSLENYEPCSSQNCSCYHGVIE
EDLTPFRGGISRKMMAEVVRRKLGHYQITKNRLYRENDCMFPSRCSGVEHFILEVIGRLPD
MEMVINVRDYPQVPKWMEPAIPVFSFSKTSEYHDIMYPAWTFWEGGPAVWPIYPTGLGRWDL
FREDLVRSAAQWPWKKKNSTAYFRGSRTSPERDPLILLSRKNPKLVDAEYTKNQAWKSMKDT
LGKPAAKDVHLVDHCKYKYLFNFREGVAASFRFKHLFLCGSLVFHVGDEWLEFFYPQLKPWVH
YIPVKTDLSNVQELLQFVKANDDVAQEIAERGSQFIRNLQMDDITCYWENLLSEYSKFLSY
NVTRRKGYDQIIPKMLKTEL

FIGURE 134

CACCCCTCCATTCTCGCCATGGCCCCTGCACTGCTCCTGATCCCTGCTGCCCTGCCTCTT
 TCATCCTGGCCTTGGCACCGGAGTGGAGTCGTGCGCTTACCTCCCTCGGCCACTTCTT
 GGAGGGATCCCAGTCTGGTGGTCCGGATGCCGCCAGGGATGGCTGGCTGCCCTGCAGGA
 CCGCAGCATCCTGCCCTGGCATGGATCTGGGCTCCTGCTTCTATTGTTGGGCAGC
 ACAGCCTCATGGCAGCTGAAAGAGTGAAGGCATGGACATCCCGTACTTGGGTCCTCAG
 AGGTCACTGTATGTGGCCTGCACTGCCCTGGCCTTGCAGCTGGTATGCGGTACTGGGAGCC
 CATAACCAAAGGCCCTGTGTTGGGAGGCTGGGCTGAGCCATGGGCCACCTGGGTGCCGC
 TCCTCTGCTTGCTCCATGTCATCTCCTGGCTCCTCATCTTAGCATCCTCTCGTCTT
 GACTATGCTGAGCTCATGGCCTCAAACAGGTATACTACCATGTGCTGGGCTGGCGAGCC
 TCTGGCCTGAAGTCTCCCCGGGCTCTCAGACTCTTCTCCCACCTGCCACCCAGTGTG
 TGGAGCTGCTGACAGTGCTGTGGTGGTGCCTACCCGGCACGGACCGTCTCCTCCTGCT
 TTCCTCCTTACCTCTACCTGGCCTGGCTCACGGCTTGATCAGCAAGACCTCCGCTACCT
 CGGGCCCAGCTACAAAGAAAATCCACCTGCTCTCGGCCACGGATGGGAGGCAGAGT
GAGGAGCTCACTGGTTACAAGCCCTGTTCTTCCCTCCCACCTGAATTCTAAATCCTTAAC
 ATCCAGGCCCTGGCTGCTCATGCCAGAGGCCAAATCCATGGACTGAAGGAGATGCCCTT
 CTACTACTTGAGACTTATTCTCTGGTCCAGCTCCATACCTAAATTCTGAGTTCA
 CTGAACCTCCAAGGTCCACTCTCACCAAGGAAGAGTGGGTATGAAAGTCATCTGCC
 TTCACTGTTAGAGCATGACACTCTCCCCCTAACAGCCTCTGAGAAGGAAAGGATCTGCC
 CTGACCACTCCCCGGACTGTTACTTGCCCTGCGCCTCAGGGTCCCCTCTGCACCGCT
 GGCTTCAACTCCAAGAAGGTGGACCAGGGTCTGCAAGTTAACGGTCAGCTGCCCTCCA
 GGCCCCAACCTGCCTCACCACTCCGGCCCTAGTCTGACACCTCCTAGGCCCTGCCT
 GGGCTCAGACCCCAACCTAGTCAAGGGATTCTCCTGCTCTTAACCGATGACTGGGCTC
 CCTGCTCTCCGAGGAAGATGCTCTGCAGGAAAATAAAAGTCAGCCTTTCTAAAAAAA

FIGURE 135

MAPALLIPIAALASFILAFGTGVEFVRFTSLRPLLGGIPESGGPDARQGWLAALQDRSILAP
LAWDLGLLLLFGVGQHSLMAAERVKAWSRYFGVLQRSLYVACTALALQLVMRYWEPIPKGPV
LWEARAEPWATWVPLLCFVLHVISWLLIFSILLVFDYAEIMGLKQVYYHVLGLGEPLALKSP
RALRLFSHLRHPCVCVELLTVLWVVPTLGTDRLLLAFLLTLYLGLAHGLDQQDLRYLRAQLQR
KLHLLSRPQDGAE

Signal sequence:

amino acids 1-13

Transmembrane domains:

amino acids 58-76, 99-113, 141-159, 203-222

N-myristoylation sites:

amino acids 37-43, 42-48, 229-235

FIGURE 136

CCGAGCACAGGAGATTGCCTGCGTTAGGAGGTGGCTGCGTTGTGGAAAAGCTATCAAGGA
 AGAAATTGCCAACCATGTCTTTCTGTTTCAGAGTAGTTACAACACAGATCTGAGTGT
 TTTAATTAAAGCATGGAATACAGAAAACAACAAAAACTTAAGCTTAATTCTGGAATT
 CCACAGTTTCTTAGCTCCCTGGACCCGGTGACCTGTTGGCTCTCCGCTGGCTGCTCTA
 TCACGTGGTGCCTCCGACTACTCACCCCGAGTGTAAAGAACCTCGGCTCGCGTGCTCTG
 AGCTGCTGTGG**ATG**GCCTCGGCTCTGGACTGTCCTCCGAGTAGGATGTCAGTGAGATCC
 CTCAAATGGAGCCTCCTGCTGTCACTCCTGAGTTCTTGTATGTTGACCTCAGCCT
 TCCCCACTACAATGTGATAAGAACGCGTGAACGGATGTACTTCTATGAGTATGAGCCGATT
 ACAGACAAGACTTCACTTCACACTCGAGAGCATTCAAACGCTCTCATCAAATCCATT
 CTGGTCATTCTGGTACCTCCCACCCTCAGATGTGAAAGGCCAGGCAGGCCATTAGAGTTAC
 TTGGGGTAAAAAAAGTCTGGTGGGATATGAGGTTCTACATTTTCTTATTAGGCCAAG
 AGGCTGAAAAGGAAGACAAAATGTTGGCATTGTCCTTAGAGGATGAACACCTCTTATGGT
 GACATAATCCGACAAGATTTTAGACACATATAAACCTGACCTGAAAACCATTATGGC
 ATTCAAGGTGGTAACTGAGTTGCCAATGCCAGTACGTAATGAAGACAGACACTGATG
 TTTCATCAATACTGGCAATTAGTGAAGTATCTTAAACCTAAACCACTCAGAGAAGTT
 TTCACAGGTTATCCTCTAATTGATAATTATTCCATAGAGGATTTACCAAAAAACCCATAT
 TTCTTACCAAGGAGTATCCTTCAAGGTGTTCCCTCCATACTGCAGTGGTTGGTTATATAA
 TGTCCAGAGATTGGTGCCAAGGATCTATGAAATGATGGTCACGTAAAACCCATCAAGTT
 GAAGATGTTATGTCGGATCTGTTGAATTATTAAAAGTGAACATTCAATTCCAGAAGA
 CACAAATCTTCTTCTATAGAATCCATTGGATGTCTGCAACTGAGACGTGTGATTG
 CAGCCCATGGCTTCTTCCAAGGAGATCATCACTTTGGCAGGTATGCTAAGGAACACC
 ACATGCCATTAT**TAA**CTTCACATTCTACAAAAGCCTAGAAGGACAGGATACCTGTGGAAA
 GTGTTAAATAAGTAGGTACTGTGGAAAATTCACTGGGAGGTCACTGCTGGCTTACACTG
 AACTGAAACTCATGAAAACCCAGACTGGAGACTGGAGGGTTACACTTGTGATTATTAGTC
 AGGCCCTCAAAGATGATATGTGGAGGAATTAAATATAAGGAATTGGAGGTTTTGCTAAA
 GAAATTAAATAGGACAAACAATTGGACATGTCATTCTGTAGACTAGAATTCTAAAAGGG
 TGTTACTGAGTTATAAGCTCACTAGGCTGTAAAAACAAAACAATGTAGAGTTTATTG
 AACAAATGTAGTCACTTGAAGGTTGTATATCTTATGTGGATTACCAATTAAAAATATA
 TGTAGTTCTGTCAAAAAACTTCTCACTGAAGTTACTGAACAAAATTACCTGTGTTT
 TGGTCATTATAAAAGTACTCAAGATGTTGCAGTATTCACAGTTATTATTAAATTA
 CTTCAACTTGTGTTTAAATGTTGACGATTCAAATACAAGATAAAAAGGATAGTGAAT
 CATTCTTACATGCAAACATTCCAGTTACTTAACGATCAGTTATTATTGATACATCAC
 TCCATTAATGTAAAGTCATAGGTCATTATTGCATATCAGTAATCTCTGGACTTTGTTAAAT
 ATTTTACTGTGGTAATATAGAGAAGAATTAAAGCAAGAAAATCTGAAAA

FIGURE 137

MASALWTVLPSRMSLRSLKWSLLLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPIYRQD
FHFTLREHSNCQNPFLVILVTSHPSDVKARQAIRVTWGEKKSSWWGYEVLTFFLLGQEAEK
EDKMLALSLEDEHLLYGDIIHQDFLDTYNNLTLKTIMAFRWVTEFCPNAKYVMKTDTDVFIN
TGNLVKYLLNLNHSEKFFTGYPLIDNYSYRGFYQKTHISYQEYPFKVFPPYCSGLGYIMSRD
LVPRIYEMMGHVVKPIKFEDVYVGICLNLLKVNIHIPEDTNLFFLYRIHLDVCQLRRVIAAHG
FSSKEIITFWQVMLRNTTCHY

FIGURE 138

CCTCTGTCCACTGCTTCGTGAAGACAAG**ATG**AAGTTACAATTGTCTTGCTGGACTTCTT
GGAGTCCTTCTAGCTCCTGCCCTAGCTAACTATAATATCAACGTCAATGATGACAACAACAA
TGCTGGAAGTGGGCAGCAGTCAGTGAGTGTCAACAAATGAACACAAATGTGGCCAATGTTGACA
ATAACAAACGGATGGGACTCCTGGAATTCCATCTGGGATTATGGAAATGGCTTGCTGCAACC
AGACTCTTCAAAAGAACATGCATTGTGCACAAATGAACAAGGAAGTCATGCCCTCCAT
TCAATCCCTTGATGCACTGGTCAAGGAAAAGAAGCTTCAGGGTAAGGGACCAGGAGGACCAC
CTCCCAAGGGCCTGATGTACTCAGTCACCCAAACAAAGTCGATGACCTGAGCAAGTCGGA
AAAAACATTGCAAACATGTGTCGTGGATTCCAACATACATGGCTGAGGAGATGCAAGAGGC
AAGCCTGTTTTACTCAGGAACGTGCTACACGACCAGTGTACTATGGATTGTGGACATTT
CCTTCTGTGGAGACACGGTGGAGA**ACTAA**ACAATTAAAGCCACTATGGATTAGTCAT
CTGAATATGCTGTGCAGAAAAAATATGGGCTCCAGTGGTTTACCATGTCATTCTGAAATT
TTTCTCTACTAGTTATGTTGATTCTTAAGTTCAATAAAATCATTAGCATTGAAAAAAA

FIGURE 139

MKFTIVFAGLLGVFLAPALANYNINVNDDNNNAGSGQQSVVNNEHNVANVDNNNGWDSWNS
IWDYGNNGFAATRLFQKKTCIVHKMNKEVMPSIQSLDALVKEKKLQGKGPGGPPKGLMYSVN
PNKVDDLSKFGKNIANMCRGIPTYMAEEMQEASLFFYSGTCYTTSVLWIVDISFCGDTVEN

Signal Peptide:

amino acids 1-20

N-myristoylation Sites:

amino acids 67-72, 118-123, 163-168

Flavodoxin protein homology:

amino acids 156-174

FIGURE 140

CATTTCTGAAACTAATCGTGTAGAATTGACTTGAAAGCATTGCTTTACAGAAAGTATA
 TTAACCTTTAGGAGTAATTCTAGTTGGATTGTAATATGAAATAATTAAAAGGGCTTCG
 CTCATATATAGGAAAATCGCATATGGCCTAGTATTAAATTCTTATTGCTTACTGATTTTT
 TGAGTTAAGAGTTGTTATATGCTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAAA
 GAATAAAGTAGATTGAGTCTCCAATTTATGTAAGCTTCAGAAGAACTGGTTGTTACATG
 CAAGCTTATAGTTGAAATATTTCAAGGAATTACATGAATGACAGTCTCGAACCAATGTGT
 TTGTTCGATTTCAACCAGAGACTATAGCATGTGCTGCATCTACCTGCAGCTAGAGCACTT
 CAGATTCCGTTGCCAACTCGTCCCCATTGGTTCTCTTTGGTACTACAGAAGAGGAAAT
 CCAGGAAATCTGCATAGAAACACTTAGGCTTATACCAGAAAAAGCCAAACTATGAATTAC
 TGGAAAAAGAAGTAGAAAAAGAAAAGTAGCCTTACAAGAACGCCAAATTAAAAGCAAAGGGA
 TTGAATCCGGATGGAACCTCCAGCCCTTCAACCCTGGGTGGATTTCTCCAGCCTCCAAGCC
 ATCATCACCAAGAGAAGTAAAGCTGAAGAGAAATCACCAATCTCCATTAATGTGAAGACAG
 TCAAAAAAGAACCTGAGGATAGACAACAGGCTCCAAAGCCCTACAATGGTGTAAAGAAAA
 GACAGCAAGAGAAGTAGAAATAGCAGAAGTGCAGTCAGTCAGGTCAAGAACACGATCACG
 TTCTAGATCACACTCCAAGAACACTATAATAATAGGCGGAGTCGATCTGGAACATACA
 GCTCGAGATCAAGAACAGGTCCCGCAGTCACAGTGAAAGCCCTCGAAGACATCATAATCAT
 GGTTCTCCTCACCTTAAGGCCAAGCATAACCAGAGATGATTTAAAAAGTTCAAACAGACATGG
 TCATAAAAGGAAAAATCTCGTTCTCGATCTCAGAGCAAGTCTCGGGATCACTCAGATGCAG
 CCAAGAAACACAGGCATGAAAGGGACATCATAGGGACAGGCGTGAACGATCTCGCTCCTT
 GAGAGGTCCCATAAAAGCAAGCACCATGGGGCAGTCGCTCAGGACATGGCAGGCACAGGCG
CTGACTTCTCTTCTTGAGCCTGCATCAGTTCTGGTTGCCTATCTACAGTGTGATGT
 ATGGACTCAATAAAAACATTAACGCAAACGTAGGATTGATTCTTGAAACCCCTCTA
 GGTCTAGAACACTGAGGACAGTTCTTGAAAGAACTATGTTAATTGTTACATTATAGT
 AAAATGCCCTAGCAGTATCTAATTAAAAACATGGTCAGGTCAATTGTTACATTATAGT
 TGTGTATTGTTATTGCTATAAGAACTGGAGCGTGAATTCTGTTAAAGATTTGTTAAATGATGGTGAAT
 ATACAGATAAAATTGCAGACACTGTTCTATTAAAGTGGTTATTGTTAAATGATGGTGAAT
 ACTTTCTTAACACTGGTTGTGCATGTGTAAAGATTTACAAGGAAATAAAATACAAAT
 CTTGTTTTCTAAAAAAAAAAAAAGT

FIGURE 141

MNDSLRTNVFVRFQPETIACACIYLAARALQIPLPTRPHWFLFGTTEEEIQEICIETRLY
TRKKPNYELLEKEVEKRKVALQEAKLKAKGLNPDGTPALSTLGGFPASKPSSPREVKAEK
SPISINVKTVKKEPEDRQQASKSPYNGVRKD SKRSRNSRSASRSRSRTRSR SRSHTPRRHYN
NRRSRSGTYSSRSRSRSRSHSESPRRHHNHGSPHLKAKHTRDDLKSSNRGHKRKKRSRSQ
SKSRDHSDAAKKHRHERGHHRDRRERSRSFERSHKSKHGGSRSGHGRHRR

FIGURE 142

TGGGGATAAAGGAAAAATGGTCAGGTATTAATGGCTAAAGATTATTGGAAGGGTTATCA
TTTTTGAAANNTATTCGGGTCANAATTGNCTTGAAAAGCATTGCTTTACAGAAATATAT
TANCTTTTAGAGTAATTCTAGTTGGATTGTAATATGAAATTATTAAAAGGGCTCGCT
CATATATAGGAAAATCGCATATGGCCTAGTATTAAATTNTTATTGCTTACTGATTTTTG
AGTTAAGAGTTGTTATATGNTAGAATATGAGGATGTGAATATAAAGAGAAGAAAAAGA
ATAAAGTAGATTGAGTCTCCAATTATGTAAGCTTCAGAAGAACTGGTTGTTACATGCA
AGCTTATAGTTGAAATATTTTCAGGAATTACATGAATGACAGTCTCGAACCAATGTGTT
GTCGATTCAACCAGAGANTATAGCATGTGCTGCATCTACCTTGCAAGNTAGAGCACTTCA
GATTCCGTTGCCAACTNGTCCCCATTGGTTCTTCTTTGGTACTACAGAAGAGGAAATCC
AGGAAATNTGCATAGAAACACTTAGGTTATACCAAGAAAAAGCCAAACTATGAATTACTG
AAAAAAGAAGTAGAAAAAGAAAAGTAGCCTACAAGAAGCCNAATTAAAAGCAAAGGGATT
GAATCCGGATGGAACTCCAGCCTTCAACCCTGGGTGGATTTCTCC

FIGURE 143

GGCACGAGGCCTCGTCCAAGCTGGCACGAGGGTGCACCGCGTTCTCGCACCGTC**ATGGC**
 GGTCCCTCGGAGTACAGCTGGTGGTACCCCTGCTCACTGCCACCCCATGCACAGGCTGGCGC
 CACACTGCTCCTCGCGCGCTGGCTGCTCTGTAACGGCAGTTGTTCCGATAAACGACACCG
 TCTGAGGAGGAGCTCGGGCCCTGGGGGAAGCCAGGGCCCAGAGGAGGAAAGAGCGGGTG
 GGCCAAATGGCCTAGTGAGGAGAACCGACTGTCTGTGCCCGAGATGCCCGTCCAGCTGG
 AGACCTGCCCTCACGACCGTGGATGCCCTGGCCTGCGCTTCCCTGGAGTACCAGTGG
 TTTGTGGACTTGCTGTACTCGGGCGCGTGTACCTCTTACAGAGGCCTACTACTACAT
 GCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGTGCCTGCTCACGGTGACCTTCT
 CCATCAAGATGTTCTGACAGTGACACGGCTGTACTTCAGCGCCGAGGAGGGGGTGAGCGC
 TCTGTCGCTCACCTTGCCTTCCCTTCCCTGCTGGCATGCTGGTGCAAGTGGTGCG
 GGAGGAGACCCTCGAGCTGGCCTGGAGCCTGGCCAGCATGACCCAGAACTTAGAGC
 CACTCTGAAGAAGCAGGGCTGGACTGGCGCTTCCGTGGCCAAGCTGGCTATCCGCGTG
 GGACTGGCAGTGGTGGCTGTGCTGGTGCCTCCTCACCTCCAGGCCTGCGGCTGGC
 CCAGACCCACCGGGACGCACTGACCATGTCGGAGGACAGACCCATGCTGCAGTCCTCC
 ACACCAGCTCCTGTCTCCCTGTTCATCCTGTGGCTCTGGACAAAGCCATTGCACGGGAC
 TTCCTGCACCAGCCGCCGTTGGGAGACGCCTTCTCCCTGCTGTCCGATTGCTTC
 CTCTGGCGCCTCTGGTGTGGCTGCTGCGCTGCTGCGGCTGGCGGTGACCCGGCCCC
 ACCTGCAGGCCTACCTGTGCCTGGCCAAGGCCGGTGGAGCAGCTGCGAAGGGAGGCTGGC
 CGCATCGAAGCCGTGAAATCCAGCAGAGGGTGGTCCGAGTCTACTGCTATGTGACCGTG
 GAGCTTGCACTGACGCCGCTCATCCTCACCCCTAACACTGCACACTTCTGCTCAAGACGC
 TGGGAGGCTATTCCCTGGGCCTGGCCCAGCTCCTACTATCCCCGACCCATCCTCAGCC
 AGCGCTGCCCATGGCTCTGGGAGGACGAAGTCCAGCAGACTGCAGCGGGATTGCCGG
 GCCCTGGGTGGCCTGCTTACTCCCTCTCCCTCCGTGGCGCTGGCCTACCTCATCTGGT
 GGACGGCTGCCAGCTGCTGCCAGCCTTCCGCTACTTCCACCAGCACTGGCA
 GGCTCC**TAG**CTGCCTGCAGACCCCTCTGGGCCCTGAGGTCTGTTCTGGGAGCGGGACA
 CTAGCCTGCCCTCTGTTGCCCGGAGGACGAGCTGCAAGGTGGGCCGGACTCCCC
 GCGCTCCCTCACCAAGTGCCTGACCCGGGCCCCCTGGACGCCAGTTCTGCTCA
 GAACTGTCTCTCCTGGGCCAGCAGCATGAGGGTCCGAGGCCATTGTCTCCGAAGCGTATG
 TGCCAGGTTGAGTGGCGAGGGTGATGCTGGCTGCTTCTGAACAAATAAGGAGCATGCC
 GATTTTAA

FIGURE 144

MAVLGVQLVVTLTATLMHRLAPHCSFARWLLCNGSLFRYKHPSEEELRALAGKPRPRGRKE
RWANGLSEEKPLSVPRDAPFQLETCPPLTVDALVLRFFLEYQWFVDFAVYSGGVYLFTTEAYY
YMLGPAKETNIAVFWCLLTFSIKMFLTVTRLYFSAEEGGERSVCLTFAFLFLLLAMLVQV
VREETLELGLEPGLASMTQNLEPLLKKQGWDWALPVAKLAIRVGLAVVGSVLGAFLTFPGLR
LAQTHRDALTMSEDRPMLQFLLHTSFLSPLFILWLWTKPIARDFLHQPPFGETRFSSLSDSA
FDSSGRWLWVVLCLLRLAVTRPHLQAYLCIAKARVEQLRREAGRIEAREIQQRVVRVYCYVT
VVSLQYLTPLILTLNCTLKLTLGGYSWGLGPAPLLSPDPSSASAAPIGSGEDEVQQTAARI
AGALGGLLTPLFLRGVLAYLIWWTAACQLLASLFGLYFHQHLAGS

FIGURE 145

CGTTNGCACGCGTCAATGGCGGTCTCGGAGTACAGCTGGTGGTACCCCTGCTCACTGCCAC
CCTCATGCACAGGCTGGCGCCACACTGCTCCTCGCGCGCTGGCTGCTCTGTAACGGCAGTT
TGTTCCGATAACAAGCACCCGTNTTGAGGAGGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCC
CAGAGGCAGGAAAGAGCGGTGGCCAATGGCCTAGTGAGGAGAAGCCACTGTCTGTGCC
GAGATGCCCGTCCAGCTGGAGACCTGCCCTCACGACCGTGGATGCCCTGGCCTGCGC
TTCTTCCTGGAGTACCAGTGGTTGTGGACTTGCTGTGTACTCGGGCGCGTGTACCTCTT
CACAGAGGCCTACTACTACATGCTGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGG
GCCTGCTCACAGTGACCTCTCCATCAAGATGTTCTGACAGTGACACGGCTGTACTTCAGC
GCCGAGGAGGGGGGTGAGCGCTCTGTCTGCCTCACCTTGCCCTTCTGCTGCTGGC
CATGCTGGTGCAAGCG

FIGURE 146

GGTTCTCATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTACGGGCCGTGATTATTAAACGTGGCTT
AATCTGAAGGTTCTCAGTCAAATTCTTGTGATCTACTGATTGTGGGGCATGGCAAGGTTGCTTAAAGGAGC
TTGGCTGGTTGGGCCCTGTAGCTGACAGAAGGTGGCCAGGGAGAATGCAGCACACTGCTGGAGA**ATGA**AAGG
CGCTTCTGTTGCTGGCTTGCTGCACTGCTAATCATTGACAATGTGGCAACCTGACTTCTG
TATTAGAACTCTGTAAGGTGCCTCCACTACGGCCTGACCAAAGATAGGAAGAGGCCTACAAGATGGCTG
TCCAGACGGCTGTGAGGCCACAGCACGGCTCCCTCCCCAGAGGTTCTGAGCTGCCACCATCTCCTAA
TGACAGACGAGCTGGCCTAGACAACCTGCCTACGTGTCCTGGCAGAGGACGGCAGCCAGCAATCAGCCC
GTGGACTCTGGCCGGAGCAACCGAACTAGGGCACGGCCCTTGAGAGATCCACTATTAGAACAGATCATTAA
AAAATAAATCGAGCTTGAGTGTCTCGAAGGACAAAGAGCAGGAGTCAGTTGCCAACCATGCGACCAGG
GCAGGGAAAATTCTGAAAACACCACTGCCCTGAAGTCTTCCAAGGTTGTAACACCTGATTCCAGATGGTGA
ATTACCAAGCATCAAGATCAATCGAGTAGATCCCAGTAAAGCCTCTATTAGGCTGGTGGAGGTAGC
CCCAGCTGGTCCATATCATTATCCAACACATTATCGTGTGATGGGTGATCGCCAGAGACGGCCGG
GAGACATCATTCTAAAGGTCAACGGGATGGACATCAGCAATGTCCTCACAACTACGCTGTGCGTCTCG
CAGCCCTGCCAGGTGCTGTGACTGTGATCGTGAACAGAAGTTCGCGCAGCAGGAACAATGGACAGGCC
GGATGCTTACAGACCCCGAGATGACAGCTTCATGTGATTCTAACAAAAGTAGCCCCGAGGAGCAGCTGGAA
TAAAATGGTGCAGGCTGGATGAGCCTGGGTTTCATCTCAATGTGCTGGATGGCGGTGTCATATCGA
CATGGTCAAGCTTGAGGAGAATGACCGTGTGTTAGGCATCAATGGACATGATCTTCGATATGCCAGGCC
TGCAGCTCATCTGATTAGGCCAGTGAAGAGCAGTGTGTTACCTCGTGTGCTGCCAGGTTCGGCAGCG
CTGACATCTTCAGGAAGCCGCTGGACAGCAATGGCAGCTGGTCCCCAGGGCAGGGAGAGGAGCAACACT
CCAAAGCCCTCCATCTAACATTACTGTCAATGAGAAGCTGGTAAATATTCAAAAGACCCGGTGAATCTCT
CGGCATGACCGTGCAGGGGAGCATCACATAGAGAATGGGATTGCTATCTATGTCATCAGTGTGAGCCC
GAGGAGTCATAAGCAGAGATGGAAGAATAAAACAGGTGACATTGTTGAATGGGATGGGTCGA
GAGGTAGCCGGAGTGGGAGCTGGCATTATGAAAAGAACATCATCCTCGATAGTACTCAA
AAAGAGTATGAGCCCCAGGAAGACTGCAGCAGGCCAGCAGGGCTGGACTCCAAC
CAAACATGGCCCCACCA
GTGACTGGTCCCCATCTGGGCTGGAATTACACGGTGTGTTAATCTGAAAGATATTGTATT
CGAAGAAACACAGCTGGAGCTGGGCTCTGATTGTAGGAGTTGAAAGAATACAATGGAAACAAACCTT
TTTCATCAAATCCATTGTTGAAGGAACACCGCATACAATGATGGAAGATTAGATGTGGTGA
CTGTCATGGTAGAAGTACATCAGGAATGATACATGCTTGTGCAAGACTGCTGAAAGAACTTAAAGGAAGA
ATTACTCTAACTATTGTTCTGGCTGGCACTTTTATTAGAATCAATGATGGGTCAGAGGAAACAGAAAAA
TCACAAATAGGCTAAGAAGTGAACACTATATTATCTGTCAGTTTATATTAAAGAAAGAACATATTGT
AAAAATGTCAAGAAAAGTATGATCATCTAACAGGCCAGTTACACCTCAGAAAATATGATT
AAACTACTAGTTTTTCACTGTGGAGGATTCTCATTACTCTAACACATTGTTATATT
AAAAAGCCCTAAACAACTAAATGATTGATTTGATACCCACTGAATTCAAGCTGATT
GGTATATGCTGAAGTCTGCCAAGGGTACATTATGCCATTTTAAATTACAGCTAA
TTGCTGAGAAACGTTGCTTCATCAAACAAAGAATAAAATATT
TTGAGAAGTTAA

FIGURE 147

MKALLLLVLPWLSPANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGCPDCASLTAT
APSPEVSAATISLMTDEPGLDNPAYVSSAEDGQPAISPVDGRSNRTRARPFERSTIRSRS
FKKINRALSVLRRTKSGSAVANHADQGRENSENTTAPEVFPRLYHLIPDGEITSIKINRVDP
SESLSIRLVGGSETPLVHIIIQHIYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRLL
ROPCQVLWLTVMREQKFRSRNNGQAPDAYRPRDDSFHVIINKSSPEEQLGIKLVRKVDEPGV
FIFNVLDGGVAYRHGQLEENDRVLAINGHDLRYGSPEAAHLIQASERRVHLVVSQRQVQRS
PDIFQEAGWNSNGSWSPGPERSNTPKPLHPTITCHEKVNNIQKDPGESLGMTVAGGASHRE
WDLPIYVISVEPGGISRDGRIKTGDILLNDGVELTEVSEAVALLKRTSSSIVLKALEV
KEYEPQEDCSSPAALDSNHNMAPPSDWSPSWVMWLELPRCLYNCKDIVLRRNTAGSLGFCIV
GGYEEYNGNKPFPIKSIVEGTPAYNDGRIRC'DILLAVNGRSTSGMIHACLRLLKELKGRI
TLTIVSWPGTFL

FIGURE 148

CCAAAGTGATCATTGAAAAAGAGATATCCACATCTCAAGCCCATAAAGGATAGAACG
GCACAGGGCAGCTTACTTACTCCAGCACCTCCTCCAGGCAA**ATG**GTGCTGACCATCT
TTGGGATACAATCTCATGGATAACGAGGTTTAACATCATCAGCCCAGCAACAATGGTGGC
AATGTTCAGGAGACAGTGACAATTGATAATGAAAAAAATACCGCCATCGTTAACATCCATGC
AGGATCATGCTCTTCTACCACAATTTGACTATAAACATGGCTACATTGCATCCAGGGTGC
TCTCCCGAAGAGCCTGCTTATCCTGAAGATGGACCACATCAGAACATCCCTCCTGAACAAAT
CTCCAATGGTACATCTATGAGAACAGGCTCTGGACAACATGTTCTCCAACAAATACACCTG
GGTCAAGTACAACCCCTCTGGAGTCTCTGATCAAAGACGTGGATTGGTCTGCTGGTCAC
CCATTGAGAAACTCTGCAAACATATCCCTTGATAAGGGGAAGTGGTGAACACACAT
AATGTCGGTGCTGGAGGCTGTGCAAAGGCTGGCTCCTGGCATCTGGGAATTCAATCTG
TGCAGACATTGATT**TAG**GATGATTAGCCCTTGTATCTTCAAAGAAATACATCC
TTGGTTACACTCAAAAGTCAAATTAAATTCTTCCAATGCCCAACTAATTTGAGATTC
AGTCAGAAAATATAATGCTGTATTTATA

FIGURE 149

MKILVAFLVVLTIFGIQSHGYEVFNIISPSNNGGNVQETVTIDNEKNTAIVNIHAGSCSSTT
IFDYKHGYIASRVLSRRACFILKMDHQNIPLNNLQWYIYEKQALDNMFSNKYTWKYNPLE
SLIKDWDWFLLGSPIEKLCKHIPLYKGEVVENTHNVGAGGCAKAGLLGILGISICADIHV

FIGURE 150

GGCACGAGCCAGGAACTAGGAGGTTCTCACTGCCCGAGCAGAGGCCCTACACCCACCGAGGC
ATGGGGCTCCCTGGCTGTTCTGCTTGGCGTGCTGGCTGCCAGCAGCTTCTCCAAGGCACG
GGAGGAAGAAATTACCCCTGTGGTCTCCATTGCCTACAAAGTCCTGGAAGTTTCCCCAAAG
GCCGCTGGGTGCTCATAACCTGCTGTGCACCCCAGCCACCACCGCCCATCACCTATTCCCTC
TGTGGAACCAAGAACATCAAGGTGGCAAGAAGGTGGTGAAGACCCACGAGCCGGCCTCCT
CAACCTCAACGTCACACTCAAGTCCAGTCCAGACCTGCTCACCTACTTCTGCCGGCGTCCT
CCACCTCAGGTGCCCATGTGGACAGTGCAGGCTACAGATGCACTGGAGCTGTGGTCCAAG
CCAGTGTCTGAGCTGCCAGGCGTCCCTCGGGCAGCCCACCTATCACCAACAGCCTGATGGGAAGGATG
GATGATCTGCCAGGCGTCCCTCGGGCAGCCCACCTATCACCAACAGCCTGATGGGAAGGATG
GGCAGGTCCACCTGCAGCAGAGACCATGCCACAGGCAGGCTGCCAACTTCTCCTCTGCCG
AGCCAGACATCGGACTGGTTCTGGTGCCAGGCTGCAAACAACGCCAATGTCCAGCACAGCGC
CCTCACAGTGGTGCCCTCAGGTGGTGAACAGAAGATGGAGGACTGGCAGGGTCCCCTGGAGA
GCCCATCCTGCCCTGCCGCTCTACAGGAGCACCCGCCGTCTGAGTGAAGAGGAGTTGGG
GGGTTCAAGGATAGGAATGGGGAGGTCAAGAGCACGCCAAGCAGCAGCCATG**TAGAATGAACC**
GTCCAGAGAGCCAAGCACGGCAGAGGACTGCAGGCCATCAGCGTGCAGTGTGTTGGTATTTGGA
GTTCATGCAAAATGAGTGTGTTAGCTGCTCTGCCACAAAAAAAAAAAAAAA

FIGURE 151

MGLPGLFCLAVLAASSFSKAREEEITPVVSIAYKVLEVFPKGRWVLITCCAPQPPPITYSL
CGTKNIKVAKKVVKTHEPASFNLNVTLKSSPDLLTYFCRASSTSGAHVDSARLQMHWELWSK
PVSELRANFTLQDRGAGPRVEMICQASSGSPPITNSLIGKDGVHLQQRPCHRQPANFSFLP
SQTSDFWCQAANNANQHSALTVVPPGGDQKMEDWQGPLESPILALPLYRSTRRLSEEEFG
GFRIGNGEVRGRKAAAM

Signal Peptide:

amino acids 1-18

N-glycosylation Sites:

amino acids 86-89, 132-135, 181-184

FIGURE 152

GGTCCCTTAATGGCAGCAGCCGCCGCTACCAAGATCCTTCTGTGCCTCCGCTTGCTCCTG
 CTGTCCGGCTGGTCCCAGGGCTGGCGAGCCGACCCCTCACTCTTTGCTATGACATCACCGT
 CATCCCTAAGTCAGACCTGGACCACGGTGGTGTGGCTCAAGGCCAGGTGGATGAAAAGA
 CTTTCTTCACTATGACTGTGGCAACAAGACAGTCACACCTGTCAGTCCCCTGGGAAGAAA
 CTAAATGTCACAACGGCCTGGAAAGCACAGAACCCAGTACTGAGAGAGGTGGTGGACATACT
 TACAGAGCAACTGCGTGACATTCAAGCTGGAGAATTACACACCCAAGGAACCCCTCACCTGC
 AGGCAAGGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTCA
 GTTCGATGGCAGATCTTCCTCCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCC
 TGGAGCCAGAAAGATGAAAGAAAAGTGGAGAATGACAAGGTTGTGGCATGTCCTTCCATT
 ACTTCTCAATGGGAGACTGTATAGGATGGCTTGAGGACTTCCTGATGGCATGGACAGCAC
 CTGGAGCCAAGTGCAGGAGCACCCTGCCATGTCCTCAGGCACAACCCAACTCAGGGCCAC
 AGCCACCACCCATCCTTGCTGCCTCCTCATCATCCTCCCTGCTCATCCTCCCTGGCA
 TCTGAGGAGAGTCCTTAGAGTGACAGGTTAAAGCTGATACCAAAAGGCTCTGTGAGCACG
 GTCTTGATCAAACCTGCCCTCTGTCTGGCAGCTGCCACGACCTACGGTGTATGTCCAGT
 GGCCCTCAGCAGATCATGATGACATCATGGACCCAATAGCTATTCACTGCCTGATTCTT
 TTGCCAACAAATTACCGAGCTTACCTAACATATTATGCAATTCTCTTGGTGTAC
 TGATGGAATTCCCTGCACTAAAGTTCTGGCTGACTAAACAAAGATATATCATTCTTCTTC
 TCTTTTGTGGAAAATCAAGTACTTCTTGAATGATGATCTCTTCTTGCAAATGATATT
 GTCAGTAAATAATCACGTTAGACTTCAGACCTCTGGGATTCTTCCGTGTGAAAGAG
 AATTTTAAATTATTAATAAGAAAAAATTATTAATGATTGTTCTTGTAAATT
 TGTTCTGTACTGATATTAAATAAGAGTTCTATTCCCCAAAAAAAAAAAAAA

FIGURE 153

MAAAAATKILLCLPLLLLGGWSRAGRDPHSLCYDITVIPKFRPGPRWCAVQQVDEKTF
HYDCGNKTVPVSPLGKKLNVTAWKAQNPVLREVVDILTEQLRDIQLENYPKEPLTLQAR
MSCEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAMSFYFS
MGDCIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLLCCLLILPCFILPGI

Important features:

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 224-246

N-glycosylation site.

amino acids 68-72, 82-86

N-myristoylation site.

amino acids 200-206, 210-216

Amidation site.

amino acids 77-81

FIGURE 154

GGGAAAGCCATTCGAAAACCCATCTATAACAACTATATATTTCTGCTGCTAGCTG
CCTTGGGCCTCACAAATTTCATTCTGTTCTGACTTCAGTTATATACCGTGGA**ATGGAG**
TTGATCCAACCATAACATCGTGGAGGGTTTAATTGGTAGCCCTCACCCATTCTG
GTGTGGCTTCTTGAGAGGATTCCACCTCAAAATCATGAACCTGGCTGTTGATCAAAA
GAGAATTGGATTCTACTCTAAAGTCATGAACTCTGGCAAAAGAAGCTAGCAGAAC
TCAACCTGGCCTCCCATAAACAGGACAGATTATTAGGTGATGGCAAAATGGATTCTACAT
CAACGGAGGCTATGAAAGCCATGAACAGATTCCAAAAAGAAAACCTCAAATTGGGAGGCCAAC
CCACAGAACAGCATTCTGGCCAGGCTG**TAA**TCAGAATTGTCGTCGATGCTAACAGC
ATTGCTTTTCCCCAAAATTAACACATTGTGGAGAAGTGATGATACTCTCCCTTACCTT
CCTCTCTCCATTCAAGCATTCAAAGTATATTTCATGAATTAAACCTTGAGCAAGGGACC
TTAGATAGGCTTATTCTGACTGTATGCTTACCAATGAGAGAAAAAAATGCATTCCGTAT
CATCCTTTCAATAAACTGTATTCAATTGAAAAAAAAAAAAAAAAAAAAAA

FIGURE 155

MELIPTITSWRVLILVVALTQFWCGFLCRGFHLQNHELWLLIKREFGFYSKSQYRTWQKKLA
EDSTWPPINRTDYSGDGKNGFYINGGYESHEQIPKRKLKGQPTEQHFWARL

FIGURE 156

GTTCTCTTCCGAGCAAATCCAGGCATGGTGAATTATGAACGTGCCACACC**ATGAAG**
 CTCTTGCGAGTACTGTGCACCACCACTGGAATGCCATCCTGCTCCGTTCGTCTA
 CCTCACGGCGCAAGTGTGGATTCTGTGCAGCCATCGCTGCTGCCGCTCAGCCGGCCCC
 AGAACTGCCCCTCCGTTGCTCGTCAGTAACCAGTTCAAGGTGGTGTGCACGCCCG
 GGCCTCTCGAGGTCCCAGGGTATTCCCTCGAACACCCGGTACCTCAACCTCATGGAGAA
 CAACATCCAGATGATCCAGGCCACACCTCCGCCACCTCCACCACCTGGAGGTCTGCAGT
 TGGCAGGAACCTCCATCCGGCAGATTGAGGTGGGGCCTCAACGGCTGGCCAGCCTAAC
 ACCCTGGAGCTGTTGACAACGGCTGACAGTCATCCCTAGGGGGCCTTGAATACTGTC
 CAAGCTGCGGGAGCTCTGGCTTCGCAACAACCCATCGAAAGCATCCCCCTTACGCCTCA
 ACCGGGTGCCCTCCCTCATGCGCTGGACTTGGGGAGCTCAAGAAGCTGGAGTATATCTCT
 GAGGGAGCTTGAGGGCTGTTCAACCTCAAGTATCTGAACCTGGGATGTGCAACATTA
 AGACATGCCAATCTCACCCCCCTGGTGGGGCTGGAGGAGCTGGAGATGTGAGGAACCACT
 TCCCTGAGATCAGGCCTGGCTCCTCCATGGCCTGAGCTCCCTCAAGAAGCTGGGTGATG
 AACTCACAGGTAGCCTGATTGAGCGGAATGCTTGACGGCTGGCTTCACTGTGGAAC
 CAACTGGCCACAATAACCTCTTCTTCCCCATGACCTCTTACCCGCTGAGGTACC
 TGGTGGAGTTGCATCTACACCAACCCCTGGAACGTGATTGTGACATTCTGGCTAGCC
 TGGTGGCTCGAGAGTATATACCCACCAATTCCACCTGCTGGCCGCTGTCATGCTCCCAT
 GCACATGCGAGGCCGCTACCTCGTGGAGGTGGACCAGGCCCTCCAGTGCCTGCCCCCT
 TCATCATGGACGCACCTCGAGACCTCAACATTCTGAGGGTCGGATGGCAGAACCTAAC
 CGGACTCCCCCTATGTCCTCGTGAAGTGGTGTGCCCCAATGGGACAGTGTGTCAGCCACGC
 CTCCGCCACCAAGGATCTGTGCTCAACGACGGCACCTGAACCTTCCACGTGCTGC
 TTTCAGACACTGGGTGTACACATGCATGGTGAACATGTTGAGGCAACTCCAACGCC
 GCCTACCTCAATGTGAGCACGGCTGAGCTAACACCTCAACTACAGCTTCTCACCACAGT
 AACAGTGGAGACCACGGAGATCTCGCCTGAGGACACAACGCGAAAGTACAAGCCTGTT
 CCACGTCCACTGGTACACATGCCGACATACACCTCTACACAGGTGCTCATTCA
 CGTGTGCCAAGCAGGTGGCAGTACCCCGACAGACACCAGTACAAGATGCAGACCAGC
 GGATGAAGTCATGAAGACCACCAAGATCATCATTGGCTGCTTGTGGCAGTGACTCTG
 CTGCCCATGTTGATTGTCTTCTATAAACTTCGTAAGCGGCCACCAGCAGCGGAGTACAG
 ACAGCCGCCGGACTGTTGAGATAATCCAGGTGGACGAAGACATCCCAGCAGCAACATCC
 AGCAGCAACAGCAGCTCGTCCGGTGTACAGGTGAGGGGGCAGTAGTGCTGCCACA
 ATGACCATATTAACACACCTACAAACCCAGCACATGGGGCCACTGGACAGAAAACAGC
 CTGGGAACTCTGCACCCACAGTCACCACTATCTGAAACCTTATATAATTCA
 TACCAAGGACAAGGTACAGGAAACTCAAATA**TGA**CTCCCCTCCCCAAAAACTTATA
 GCAATAGAATGCACACAAAGACAGCAACTTTGTACAGAGTGGGGAGAGACTTTCTG
 TATGCTTATATATTAAGTCTATGGCCTGGTAAAAAAACAGATTATATTAA
 CAAAAAGTCAAAACA

FIGURE 157

MKLLWQVTVHHHTWNAILLPFVYLTAQVWILCAAIAAAASAGPQNCPSCSNSNQFSKVVC
RRGLSEVPQGIPSNTRYLNLMENNIQMIQADTFRHLHLEVLQLGRNSIRQIEVGAFNGLAS
LNTLELFDNWLTVIPSGAFEYLSKLRELWLRNNPIESIPSYAFNRVPSLMRLDLGELKKLEY
ISEGAFEGLFNLKYLNLCMCNIKDMPNLTPLVGLEELEMMSGNHFPEIRPGSFHGLSSLKKLW
VMNSQVSLIERNAFDGLASLVELNLAHNNLSSLPHDLFTPLRYLVELHLHHNPWNCDCDILW
LAWWLREYIPTNSTCCGRCHAPMHMRGRYLVEVDQASFQCSAPFIMDAPRDLNISEGRMAEL
KCRTPPMSSVKWLLPNGTVLSHASRHPRISVLNDGTNFHVLLSDTGVYTCMVNVAGNSN
ASAYLNVSTAELNTSNYSFFTTVTVETTEISPEDTRKYKPVPTTSTGYQPAYTTSTTVLIQ
TTRVPKQVAVPATDTTDKMQTSLEVMKTKIIIGCFVAVTLLAAAMLIVFYKLRKRHQQRS
TVTAARTVEIIQVDEDIPAATSAAATAAPSGVSGEAVVLPТИHDHINYNTYKPAHGAHWTE
NSLGNSLHPTVTTISEPYIIQTHTKDKVQETQI

FIGURE 158

CGCTCGGCACCAGCGCGCAAGG**ATGGAGCTGGTTGCTGGACGCAGTGGGGCTCACTTTCTTCAGCTCC**
 TTCTCATCTCGTCCTTGCCAAGAGAGTACACAGTCATTAAATGAAGCCTGCCCTGGAGCAGAGTGGAAATATCATG
 TGTCGGGAGTGTGAATATGATCAGATTGAGTCGCTGCCCCGGAAGAGGGAAGTCGTGGGTATACCAT
 CCCTTGCTGCAGGAATGAGGAGAATGAGTGTACTCCTGCCTGATCCACCCAGGTTGTAACATTTGAAA
 GCAAGAGCTGCCAATGGCTATGGGGGGTACCTTGGATGACTCTATGTGAAGGGGTTCTACTGTGCAGAG
 TGCCGAGCAGGCTGGTACGGAGGAGACTGCATGCGATGTGCCAGGTTGCGAGGCCAAAGGGTCAGATTT
 GTTGGAAAGCTATCCCCTAAATGCTACTGTGAATGGACCATTCATGCTAAACCTGGGTTGTCATCCA
 ACTAA
 GATTGTGATGTTGAGTCTGGAGTTGACTACATGTGCCAGTGTGACTATGTTGAGGTTGATGGAGAAC
 CGCGATGCCAGATCATCAAGCTGTCTGGCAACAGGGCCAGCTCTATCCAGAGCATAGGATCCTCA
 CCACGTCTCTCCACTCCGATGGCTCAAGAATTTCAGCGTTCCATGCCATTATGAGGAGATCACAGCAT
 GCTCCTCATCCCCTGTTCCATGACGGCACGTCGCTCCTGACAAGGCTGGATCTACAAGTGTGCCTGCTTG
 GCAGGCTATACTGGCAGCCTGTGAAAATCTCCTGAGAAAGAAACTGCTCAGACCCCTGGGGCCAGTCAA
 TGGTACAGAAAAAAACAGGGGCCCTGGCTTATCAACGGACGCCATGCTAAAATTGGCACCGTGGTGTCTT
 TCTTTGTAACAACCTATGTTCTTAGTGGCAATGAGAAAAGAACTTGCACAGCAGAATGGAGAGTGGTCAGGG
 AACAGCCCATCTGCATAAAAGCCTGCCAGAACCAAAGATTCAAGACCTGGTGAGAAGGGAGAGTTCTCCGAT
 GCAGGTTCAAGGGAGACACCATTACACCAGCTATACTCAGCGGCCTCAGCAAGCAGAAACTGCAGAGTG
 CCCCTACCAAGAACGCCAGCCCTTCCCTTGGAGATCTGCCATGGGATACCAACATTCGATACCCAGCTCCAG
 TATGAGTGCATCTCACCTCTACCGCCGCTGGGCAGCAGCAGGAGACATGTCAGGGACTGGGAAGTGGAG
 TGGCGGGCACCATCCTGCATCCCTATCTGCCGGAAAATTGAGAACATCACTGCTCAAAGACCAAGGGTTGC
 GCTGGCGTGGCAGGCAGCCATCTACAGGAGGACCAGCGGGGTGCATGACGGCAGCCTACACAAGGGAGCGTGG
 TTCCTAGTCTGCAGCGGTGCCCTGGTGAATGAGCGACTGTGGTGGTGGCTGCCACTGTGTACTGACCTGGG
 GAAGGTACCATGATCAAGACAGCAGACCTGAAAGTTGTTGGGAAATTCTACCGGATGATGACCGGAGT
 AGAACGACATCCAGAGCCTACAGATTCTGCTATCATTCTGCATCCAACTATGACCCCATCCTGCTTGATGCT
 GACATGCCATCCTGAAGCTCTAGACAAGGCCGTATCAGCACCCGAGTCCAGCCCATCTGCCCTCGCTGCCAG
 TCGGGATCTCAGCACTCCTCCAGGAGTCCCACATCACTGTGGTGGCTGGGAATGTCCTGGCAGACGTGAGGA
 GCCCTGGCTCAAGAACGACACACTGCGCTCTGGGTGGTCAGTGTGGTGGACTCGCTGCTGTGAGGAGCAG
 CATGAGGACCATGCACTCCCACTGAGTGTCACTGATAACATGTTCTGCGGAGCTGGGAACCCACTGCCCTTC
 TGATATCTGCACTGCAGAGACAGGAGGACATGCCGCTGTGTCCTCCGGACGAGCATCTCTGAGCCACGCT
 GGCACTGATGGGACTGGTCAGCTGGAGCTATGATAAAACATGAGCCACAGGCTCTCACTGCCCTCACCAAG
 GTGCTGCCCTTAAAGACTGGATTGAAAATGAAATGAAAT**TGA**ACCATGCTCATGCACTCCATTGAGAAGTGTTC
 TGTATATCCGCTGTACGTGTCAATTGCGTGAAGCAGTGTGGCCTGAAGTGTGATTGCGCTGTGAACCTGG
 CTGTCGCAAGGGCTCTGACTTCAGGGACAAAATCAGTGAAGGGTGAAGTGAACCTCATTGCTGGTAGGCTGAT
 GCCCGTCCACTACTAGGACAGCAATTGGAAGATGCCAGGGCTTGAAGAAGTAAGTTCTCAAAGAAC
 ATATACAAAACCTCTCACTCCACTGACCTGGTGGCTTCCCCACTTCACTGAGTTACGAATGCCATCAGCTG
 ACCAGGGAGATCTGGCTTCAAGGGCCCTTTGAGGCTCTCAAGTTCTAGAGAGCTGCCTGGGACAGCC
 CAGGGCAGCAGAGCTGGGATGTTGTCATGCCCTTGTGACATGCCACAGTACAGTGTGGCTTCC
 CCATCTCTGTACACATTAAATAAGGGTGGCTCTGAACACTACAAAAAAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAA

FIGURE 159

MELGCWTQLGLTFLQLLLISLPPREYTVINEACPGAEWNIMCRECCEYDQIECVCPGKREVV
GYTIPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGTLDDFYVKGFYCAECRAGWYGGD
CMRCGQVLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRD
GDNRDGQIIKRVCGNERPAPIQSIGSSLHVLFHSDGSKNFDGHAIYEEITACSSSPCFHDG
TCVLDKAGSYKCACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTV
VSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISDLVRRRVLPMQVSRETPLH
QLYSAAFSKQKLQSAPTKKPALPFGDLPMDYQHLHTQLQYECISPFYRLGSSRTCLRTGK
WSGRAPSCIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAFLVCSGALVNE
RTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYRDDRDEKTIQSLQISAIILHPNYDPILL
ADIAITLKLKDARISTRVQPICLAASRDLSTSFOESHITVAGWNVLADVRSPGFKNDTLRSG
VVSVVDSLLCEEQHEDHGIPVSVDNMFCASWEPTAPSdictaetGGIAAVSFPGRASPEPR
WHLMGLVWSWSYDKTCSHRLSTAFTKVLPFKDWIERNMK

FIGURE 160

ACCAGGCATTGTATCTTCAGTTGTCATCAAGTTCGCAATCAGATTGGAAAAGCTCAACTTGA
 AGCTTTCTTGCCTGCAGTGAAGCAGAGAGATAGATATTACCGTAATAAAAAC**ATGGGC**
 TTCAACCTGACTTCCACCTTCCTACAAATTCCGATTACTGTTGCTGTTGACTTGTGCC
 GACAGTGGTTGGGTGGGCCACCAGTAACTACTTCGTTGGTGCCTACAGAGAGATTCTAAAG
 CAAAGGAGTTCATGGCTAATTCCATAAGACCCTCATTGGGAAGGGAAAAACTCTGACT
 AATGAAGCATCCACGAAGAAGGTAGAACTTGACAACGTGCTTCTGTGTCCTTACCTCAG
 AGGCCAGAGCAAGCTCATTTCAAACCAAGATCTCACTTGGAAGAGGTACAGGCAGAAAATC
 CCAAAGTGTCCAGAGGCCGGTATGCCCTCAGGAATGTAAGCTTACAGAGGGTCGCCATC
 CTCGTTCCCCACCGGAACAGAGAGAACACCTGATGTACCTGCTGGAACATCTGCATCC
 CCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCACTCACCAGGCTGAAGGTAAAAGT
 TTAATCGAGCCAAACTCTGAATGTGGCTATCTAGAACGCCCTCAAGGAAGAAAATTGGGAC
 TGCTTATATTCCACGATGTGGACCTGGTACCGAGAATGACTTAAACCTTACAAGTGTGA
 GGAGCATCCCAAGCATCTGGTGGTGGCAGGAACAGCACTGGTACAGGTTACGTTACAGTG
 GATATTGGGGGTGTTACTGCCCTAACGAGAGAGCAGTTCAAGGTGAATGGATTCT
 AACAACTACTGGGATGGGGAGGGCGAACAGCAGTGAACCTCAGACTCAGGGTGAGCTCAAAG
 AATGAAAATTCCCGCCCTGCCCTGAAGTGGTAAATATAACATGGCTTCCACACTAGAG
 ACAAAAGGCAATGAGGTGAACGCAGAACGGATGAAGCTTACACCAAGTGTACGAGTC
 AGAACAGATGGGTGAGTAGTTCTTATAAATTAGTATCTGTGGAACACAATCCTTATA
 TATCAACATCACAGTGGATTCTGGTTGGTGCAT**TGA**CCCTGGATCTTGGTATGTTGG
 AAGAACTGATTCTTGGTGCATAATTGGCTAGAGACTCAAATAGTAGCACACATTA
 AGAACCTGTTACAGCTCATTGGTAGCTGAATTTCCTTTGTATTTCTTAGCAGAGCT
 CCTGGTATGTAGAGTATAAACAGTTGTAACAAAGACAGCTTCTTAGTCATTGGATCATG
 AGGGTTAAATATTGTAATATGGTACCTGAGGACTTATATAAAAGGATGACTCAAAGGAT
 AAAATGAACGCTATTGAGGACTCTGGTGAAGGGAGATTATTAAATTGAAGTAATATAT
 TATGGATAAAAGGCCACAGGAAATAAGACTGCTGAATGTCTGAGAGAACAGAGTTCT
 CGTCCAAGGTAGAAAGGTACGAAGATAACAATACTGTTATTCACTTACATCT
 GTGAAGTGGTGGTGCAGGTGAGAACGGCGTCCACAAAAGAGGGAGAAAAGGCACGA
 GGACACAGTGAACCTGGGAATGAAGAGGTAGCAGGAGGGTGGAGTGTGGCTGCAAAGG
 CAGTAGCTGAGCTGGTGCAGGTGCTGATAGCCTCAGGGGAGGACCTGCCAGGTATGC
 TCCAGTGATGCCACCAGAGAATACATTCTCTATTAGTTAAAGAGTTGTAAAATGA
 TTTTGTAACAGTAGGATATGAATTAGCAGTTACAAGTTACATATTAACATAAAATA
 TGTCTATCAAATACCTCTGTAGAAAATGTGAAAAGCAAA

FIGURE 161

MGFNLTFHLSYKFRLLLLLTLCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLLGKGKT
LTNEASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYRPQECKALQRV
AIVPVRNREKHLMYLLEHLHPFLQRQQLDYGIYVIHQAEKKFNRAKLLNVGYLEALKKEN
WDCFIFHDVDLVPENDFNLYKCEEHPKHLVVGRNSTGYRLRSGYFGGVTA
LSREQFFKVNGFSNNYWGWGGEDDDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSR
VWR TDGLSSCSYKLVSVEHNPLYINITVDFWFAGA

Important features:

Signal peptide:

amino acids 1-27

N-glycosylation sites:

amino acids 4-7, 220-223 and 335-338

Xylose isomerase proteins:

amino acids 191-201

FIGURE 162

CGTGGGCCGGGTCGCGCAGCGGGCTGTGGCGGCCGGAGGAGCACCAGCTCT
 GAGCTCAGCTGCATTCCCTCCGCGTCCGCCACGCTTCTCCGCTCCGGCCCCGCA**ATG**
 GCCCAGGCAGTGTGGTCGCGCTCGGCCGATCCTCTGGCTTGCCTGCCTCTGCCCTGGC
 CCCGGCAGGGTGGCGCAGGCCTGTATGAACATCAATCTACCCACCGATAGCCCTGCCACCA
 CGGGAGCGGTGGTGACCATCTCGGCCAGCCTGGTGGCAAGGACAACGGCAGCCTGGCCCTG
 CCCGCTGACGCCACCTACCGCTTCACTGGATCCACACCCCGTGGTGTACTGGCAA
 GATGGAGAAGGGTCTCAGCTCACCATCCGTGTGGTGGCCACGTGCCGGGGATTCCC
 TCTCTGTCTGGGTCACTGCCGCTGACTGCTGGATGTGCCAGCCTGTGGCCAGGGCTTGTG
 GTCTCTCCCCTACAGAGTTCTCGTGGGGACCTTGTGTACCCAGAACACTTCCCTACC
 CTGGCCCAGCTCCTATCTACTAAAGACCGTCTGAAAGTCTCCTCCACGACCCGA
 GCAACTCCTCAAGACCGCCTGTTCTACAGCTGGACTTCGGGACCTCACCAGAAGCT
 GTGACTGAAGACTCCGTGGTCTATTATAACTATTCCATCATGGGACCTCACCAGAAGCT
 CAAAGTGGTGGCGGAGTGGGAAGAGGTGGAGGCCGGATGCCACGAGGGCTGTGAAGCAGAAGA
 CGGGGACTTCTCCGCCTCGCTGAAGCTGCAGGAAACCTCGAGGCATCCAAGTGTGGG
 CCCACCTTAATTCAAGACCTTCAAAAGATGACCGTGACCTGAACTTCTGGGGAGCCCTCC
 TCTGACTGTGTGCTGGCGTCTCAAGCCTGAGTGCCCTCCGCTGGAGGAAGGGAGTGCCACC
 CTGTGTCCGTGGCCAGCACAGCTACAACCTGACCCACACCTCAGGGACCCCTGGGGACTAC
 TGCTTCAGCATCCGGGCCAGAATATCATCAGCAAGACACATCAGTACCAACAGATCCAGGT
 GTGGCCCTCCAGAATCCAGCCGGTGTCTTGTCTTCCATGTGCTACACTTATCACTGTGA
 TGTTGGCCTTCATCATGTACATGACCTGCGGAATGCCACTCAGCAAAGGACATGGTGGAG
 AACCCGGAGCCACCTCTGGGTCAAGGTGCTGCCAGATGTGCTGTGGCCTTCTGCT
 GGAGACTCCATGTGAGTACCTGGAAATTGTTGTGAGAACACGGGCTGCTCCGCCCTCT
 ATAAGTCTGTCAAAACTACACCGTGT**TGA**GCACTCCCCCTCCCCACCCATCTCAGTGTAA
 CTGACTGCTGACTTGGAGTTCCAGCAGGGTGGTGTGCACCACTGACCAAGGAGGGTTCATT
 TGCCTGGGGCTGTGGCTGGATCATCCATCTGTACAGTCCAGCCACTGCCACAAGCC
 CCTCCCTCTGTCAACCCCTGACCCAGCATTACCCATCTGTACAGTCCAGCCACTGACA
 TAAGCCCCACTCGGTTACCACCCCTTGACCCCTACCTTGAAGAGGGCTCGTAGGACT
 TTGATGCTTGGGTGTTCCGTGTTGACTCTAGGTGGCCTGGCTGCCACTGCCATTCT
 CTCATATTGGCACATCTGCTGTCCATTGGGGTTCTCAGTTCTCCCCCAGACAGCCCTAC
 CTGTGCCAGAGAGCTAGAAAGAAGGTCTAAAGGGTAAAAATCCATAACTAAAGGTTGTAC
 ACATAGATGGGACACTCACAGAGAGAAGTGTGCATGTACACACACCACACACACA
 CACACACACAGAAATATAACACATGCGTCACATGGCATTTCAGATGATCAGCTGT
 TCTGGTTAAGTCGGTTGCTGGATGCACCCCTGCACTAGAGCTGAAAGGAAATTGACCTCCA
 AGCAGCCCTGACAGGTTCTGGGCCGGCCCTCCCTTGCTGCTCTGCAGTTCTGC
 GCCCTTATAAGGCCATCTAGTCCCTGCTGGCTGGCAGGGCCTGGATGGGGCAGGACT
 AATACTGAGTGATTGCAGAGTGCTTATAATATCACCTATTTATCGAAACCCATCTGTG
 AAACCTTCACTGAGGAAAAGGCCTTGCAGCGGTAGAAGAGGGTTGAGTCAAGGCCGGCG
 TGGCTCACGCCTGTAATCCCAGCACTTGGGAGGCCAGGGCGGGTGGATCACGAGATCAGGA
 GATCGAGACCAACCTGGCTAACACGGTGAACACCCGTCTACTAAAAAAATACAAAAAGTT
 AGCCGGCGTGGTGGTGGTGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATG
 GTGCGAACCCGGGAGGCGGAGCTGCAGTGAGCCAGATGGGCCACTGCACCTCAGCCTGA
 GTGACAGAGCGAGACTCTGTCTCCA

FIGURE 163

MAQAVWSRLGRILWLACLLPWAPAGVAAGLYELNLTTDSPATTGAVVTISASLVAKDNGSLA
LPADAHLYRFHWIHTPLVLTGKMEKGLSSTIRVVGHVPGEFPVS梧TAADCWMCQPVARGF
VVLPITEFLVGDLVVTQNTSLPWPSYLTKTVLKVSFLLHDPSNFLKTALFLYSWDFGDGTQ
MVTEDSVVYYNYSIIGTFTVKLKVAEWEVEPDATRAVKQKTGDFSASLKLQETLRGIQVL
GPTLIQTTFQKMTVTLNFLGSPPLETVCWRLLKPECLPLEEGECHPVSVASTAYNLHTFRDPGD
YCFSIRAENIISKTHQYHKIQVWPSRIQPAVFATCATLITVMLAFIMYMTLRNATQQKDMV
ENPEPPSGVRCCCQMCCGPFLLETPSEYLEIVRENHGLLPPLYKSVKYTV

Important features of the protein:

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 339-362

N-glycosylation sites.

amino acids 34-37, 58-61, 142-145, 197-200, 300-303 and 364-367

FIGURE 164

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACG**ATG**GCAC TGAGCTCCCAGATCT
GGGCCGCTTGCCCTCGCTCCTCCTCCTCGCCAGCCTGACCAGTGGCTCTGTTTCCA
CAACAGACGGACA**ACTT**GCAGAGCTGCAACCCAGGACAGAGCTGGAGCCAGGGCCAGCTG
GATGCCCATGTTCCAGAGGCGAAGGAGGCGAGACACCCACTTCCCCATTCGATTTCTGCT
GCGGCTGCTGTATCGATCAAAGTGTGGGATGTGCTGCAAGACG**TAGA**ACCTACCTGCCCTG
CCCCCGTCCCCTCCCTCCTTATTATTCTGCTGCCAGAACATAGGTCTTGGAAATAAAA
TGGCTGGTTCTTTGTTCCAAAAA
AAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 165

MALSSQIWAACLLLLL~~ASLTGSVFPQQTGQLAELOPQDRAGARASWMPMFQRRRRDTH~~
FPICIFCCGCCHR~~SKCGM~~CCKT

FIGURE 166

CTGTCAGGAAGGACCATCTGAAGGCTGCAATTGTTAGGGAGGCAGGTGCTGGCCTGGC
 CTGGATCTTCCACC**ATG**TCTGCTGCCTTTGATAGCCTGATTGTCAACCTCTGGGC
 ATCTCCCTGACTGTCCTCTCACCCCTCTCGTTTCATCATAGTCCAGCCATTGG
 AGTCTCCTTGGTATCCGCAAACCTACATGAAAAGTCTGTTAAAATCTTGCGTGGGCTA
 CCTTGAGAATGGAGCGAGGAGCCAAGGAGAAGAACCAACAGCTTACAAGCCCTACACCAAC
 GGAATCATTGCAAAGGATCCCACCTCACTAGAAGAAGAGATCAAAGAGATTGTCGAAGTGG
 TAGTAGTAAGGCTCTGGACAAACACTCCAGAGTTCGAGCTCTGACATTTCACCTTGCC
 GGAAAGGAATGGAGACCAATTGGATGATGAGGTGACAAAGAGATTCTCAGCAGAAGAACTG
 GAGTCCTGGAACCTGCTGAGCAGAACCAATTATAACTCCAGTACATCAGCCTCGGCTCAC
 GGTCTGTGGGGTTAGGAGTGCTGATTGGTACTGCTTCTGCTGCCGCTCAGGATAGCAC
 TGGCTTCACAGGGATTAGCCTCTGGTGGTGGCACAACTGTGGTGGGATACCTGCCAAT
 GGGAGGTTAAGGAATTGAGTAAACATGTTACTTAATGTGTTACCGGATCTGCGTGC
 AGCGCTGACAGCCATCATCACCTACCATGACAGGGAAACAGACCAAGAAATGGTGGCATCT
 GTGTGGCCAATCATACCTCACCGATCGATGTGATCATCTGGCCAGCGATGGCTATTATGCC
 ATGGTGGGTCAAGTGCACGGGGACTCATGGGTGTGATTGAGAGGCCATGGTGAAGGCCTG
 CCCACACGTCTGGTTGAGCGCTCGGAAGTGAAGGATGCCACCTGGTGGCTAAGAGACTGA
 CTGAACATGTGCAAGATAAAAGCAAGCTGCCATCCTCATCTCCCAGAAGGAACCTGCATC
 AATAATACATCGGTGATGATGTTCAAAAAGGGAAAGTTTGAAATTGGAGGCCACAGTTACCC
 TGTTGCTATCAAGTATGACCCCTCAATTGGCGATGCCCTCTGGAACAGCAGCAAATACGGG
 TGGTGACGTACCTGCTGCAATGATGACCAGCTGGCCATTGTCTGCGAGCGTGTGGTACCTG
 CCTCCCATGACTAGAGAGGGCAGATGAAGATGCTGCCAGTTGCGAATAGGGTGAATCTGC
 CATTGCCAGGCAGGGAGGACTTGTGGACCTGCTGTGGATGGGGCTGAAGAGGGAGAAGG
 TGAAGGACACGTTCAAGGAGGAGCAGCAGAAAGCTGTACAGCAAGATGATCGTGGGAACCC
 AAGGACAGGAGCCGCT**TGA**GCCTGCCCTCAGCTGGCTGGGCCACCGTGCAGGGTGC
 CGGGCTCAGAGCTGGAGTTGCCGCCGCCGCCCCACTGCTGTGCTCTTCCAGACTCCAGGG
 CTCCCCGGGCTGCTCTGGATCCCAGGACTCCGGCTTCGCCAGCCGAGCGGGATCCCTGT
 GCACCCGGCGCAGCCTACCCCTGGTGGCTAAACGGATGCTGCTGGTGTGCGACCCAGGA
 CGAGATGCCATTGTTCTTACAATAAGTCGTTGGAGGAATGCCATTAAAGTGAACCTCCCC
 CCTTGACGCTGTGCGGGCTGAGTGGTTGGGAGATGTGGCATGGCTTGTGCTAGAGAT
 GGCAGGCTACAAGAGTCTGTTATGCAAGCCGTGTGCCAGGGATGTGCTGGGGCGGCCACCC
 CTCTCCAGGAAAGGCACAGCTGAGGCAGTGTGGCTGGCTGCCCTAACATGCCAGG
 CTTGGAGCTGCAAGACATGATAGGAAGGAAACTGTCATCTGCAGGGCTTCAGCAAATG
 AAGGGTTAGATTTATGCTGCTGATGGGTTACTAAAGGGAGGGGAAGAGGCCAGGTG
 GGCGCTGACTGGGCCATGGGAGAACGTGTGTTCTGACTCCAGGCTAACCTGAACCTCCC
 ATGTGATGCGCTTGTGAATGTTGCTCGGTTCCCCATCTGTAATATGAGTCGGGG
 GAATGGTGGTGAATCCTACCTCACAGGGCTGTTGGGGATAAAGTGTGCTGCCAGGGTGA
 AGGACACATCACGTTCAAGTACAGGCCACAAACGGGGCACGGCAGGCCTGAG
 CTCAGAGCTGCACTGGCTTGGATTGTTCTGAGTAAATAACTGGCTGGTGA
 TGA

FIGURE 167

MFLLLPFDSLIVNLLGISLTVLFTLLLVIIVPAIFGVSGIRKLYMKSLKIFAWATLRME
RGAKEKNHQLYKPYTNGIIAKDPTSLEEEIKEIRRSGSSKALDNTPEFELSDIFYFCRGME
TIMDEVTKRFSAAELESWNLLSRTNYNFQYISLRLTVLWGLGVLIRYCFLPLRIALAFG
ISLLVVGTTVVGYLPNGRFKEFMSKHLMCYRICVRALTIAITYHDRENPRNGGICVANH
TSPIDVIILASDGYYAMVGQVHGGLMGVIQRAMVKACPHWWFERSEVKDRHLVAKRLTEHVQ
DKSKLPILIFPEGTCINNTSVMMFKKGSFEIGATVYPVAIKYDPQFGDAFWNSSKYGMVTYL
LRRMMTSWAIVCSVWYLPPMTREADEDAVQFANRVKSAIARQGGLVDLWDGGLKREKVKDTF
KEEQOKLYSKMIVGNHKDRSRSG

FIGURE 168

GCCCCTCGAAACCAGGACTCCAGCACCTCTGGTCCCAGCCTCACCCGGACCCCTGGCCCTCA
 CGTCTCCTCCAGGG**ATG**GCGCTGGCGGCTTGATGATGCCCTCGGCAGCCTGGCCTCCAC
 ACCTGGCAGGCCAGGCTGTTCCCACCATCCTGCCCTGGGCTGGCTCCAGACACCTTGAG
 CGATACTATGTGGGTTGTGCAGAGGAGATGGAGGAGAAGGCAGCCCCCTGCTAAAGGAGG
 AAATGGCCCACCAGGCCCTGCTGCCGAATCCTGGGAGGCAGCCCAGGAGACCTGGGAGGAC
 AAGCGTCGAGGGCTTACCTTGCCCCCTGGCTCAAAGCCCAGAATGGAATAGCCATTATGGT
 CTACACCAACTCATCGAACACCTTGTACTGGGAGTTGAATCAGGCCGTGCGGACGGCGGAG
 GCTCCCGGGAGCTCTACATGAGGCACCTTCCCTCAAGGCCCTGCATTCTACCTGATCCGG
 GCCCTGCAGCTGCTGCGAGGCAGTGGGGCTGCAGCAGGGACCTGGGAGGTGGTGGTCCG
 AGGTGTGGCAGCCTCGCTTGAACCCAAGAGGCTGGGGACTCTGTCCGCTGGCCAGT
 TTGCCTCCAGCTCCCTGGATAAGGCAGTGGCCACAGATTGGGGAGAAGAGGCCGGCTGT
 GTGTCTGCGCCAGGGTGCAGCTAGGGTCACAATCTGAGGGGCCTCTCTGCCCTG
 GAAGACTCTGCTCTGGCCCTGGAGAGTCCAGCTCTCAGGGTTGGCCC**TGA**AAGTCCA
 ACATCTGCCACTTAGGAGCCCTGGAACGGTGACCTCATATGACGAAGAGGCACCTCCAG
 CAGCCTTGAGAAGCAAGAACATGGTCCGGACCCAGCCCTAGCAGCCTCTCCCCAACAGG
 ATGTTGGCCTGGGGAGGCCACAGCAGGGCTGAGGGAACTCTGCTATGTGATGGGACTTCCT
 GGGACAAGCAAGGAAAGTACTGAGGCAGCCACTTGATTGAACGGTGTGCAATGTGGAGACA
 TGGAGTTTATTGAGGTAGCTACGTGATTAAATGGTATTGCAGTGTGGA

FIGURE 169

MALAALMIALGSLGLHTWQAQAVPTILPLGLAPDTFDDTYVGCAEEMEEKAAPLLKEEMAH
ALLRESWEAAQETWEDKRRGLTLPPGFKAQNGIAIMVYTNSNTLYWELNQAVRTGGGSREL
YMRHFPFKALHFYLIRALQLLRGSGGCSRGPGEVVFRGVGSLRFEPKRLGDSVRLGQFASSS
LDKAVAHRFGEKRRGCVSAPGVQLGSQSEGASSLPPWTLLAPGEFQLSGVGP

FIGURE 170

GTCGGTTCCGTTGGTGGGCCGTGACTTCCCCCTGAAGTCAAAGTAAAGCAAGTTGACTCTATTGTCTGGACCTTCAACACAACCCCTTTGTCAACCATAACAGCCAGAAGGGGCACATATCACTAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTACTCCCTGAAGCTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGACCAATCTGACATGCTGCATGGAACATGGGAAGAGGATGTGATTATACCTGGAAGGCCCTGGGCAAGCAGCCAATGAGTCACATAATGGGTCCATCCTCCCCATCTCCTGGAGATGGGAGAAAGTGATATGACCTTCATCTGCCTGCCAGGAACCCCTGTCAGCAGAAACTCTCAAGCCCCATCCTGCCAGGAAGCTCTGTAAGGTGCTGATGACCCAGATTCCCTCATGGTCCTCCTGTGTCTCCTGTTGGTGCCCTCCTGCTCAGTCTTTGACTGGGCTATTCTTGTTCTGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTAGGACATTGTCGGAAACTCCTAACATATGCCCATCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAATAGAACAACTCTAAAGGAAGATCCAGCAAATACGGTTACTCCACTGTGGAAATACCGAAAAAGATGGAAAATCCCCACTCACTGCTCACGATGCCAGACACACCAAGGCTATTGCCTATGAGAATGTTATC**TAG**ACAGCAGTCACACTCCCTAACGTCTGCTCA

FIGURE 171

MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLSKVKQVDSIVWTFNTTPLVT
IQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHV
YEHLSKPVMTMGLQSNKNGTCVTNLTCMEHGEEDVIYTWKALGQAANESHNGSILPISWRW
GESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLVPLLLSLFVLGLFLW
FLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPANTVYSTVEIP
KKMENPHSLLTMDTPRLFAYENVI

FIGURE 172

CTGGTTCCCCAACATGCCTCACCTCATCTATCCTTGGCAGCTCACAGGGTCAGCAGCC
TCTGGACCGTGAAAGAGCTGGTCGGTCCGGTGGTGGGCCGTGACTTCCCCTGAAGTC
CAAAGTAAAGCAAGTTGACTCTATTGTCTGGACCTCAACACAACCCCTCTTGTCAACCATA
AGCCAGAAGGGGGCACTATCATAGTGACCCAAATCGTAATAGGGAGAGTAGACTTCCA
GATGGAGGCTACTCCCTGAAGCTCAGCAAATGACTGAAGAAGAATGACTCAGGGATCTACTATGT
GGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACG
AGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTG
ACCAATCTGACATGCTGCATGGAACATGGGAAGAGGATGTGATTATACCTGGAAGGCCT
GGGCAGCAGCCAATGAGTCCCATAATGGGTCCATCCTCCCCATCTCCTGGAGATGGGAG
AAAGTGATATGACCTTCATCTGGTGTGCCAGGAACCCGTCAAGCAGAAACTTCTCAAGCCCC
ATCCTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCCCTCCATGGTCCTCCT
GTGTCTCCTGTTGGTGCCCTCCTGCTCAGTCTTGTACTGGGCTATTCTTGGTTTC
TGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTGTCGGAA
ACTCCTAACATATGCCCTATTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAA
TAGAACAAATCCTAAAGGAAGATCCAGCAAATACGGTTACTCCACTGTGGAAATACCGAAAA
AGATGGAAAATCCCCACTCACTGCTCACGATGCCAGACACACCAAGGCTATTGCCTATGAG
AATGTTATCTAGACAGCAGTGCACTCCCCTAAGTCTGTCTCAAAAAAAAAAAAAAA

FIGURE 173

GAAAGACGTGGCCTGACAGACAGACAATCCTATTCCCTACCAAA**ATG**AAGATGCTGCTGCT
GCTGTGTTGGACTGACCCTAGTCTGTCCATGCAGAAGAAGCTAGTTCTACGGGAAGGA
ACTTTAACATGAGAAAAGATTAATGGGAATGGCATACTATTATCCTGGCCTCTGACAAAAGA
GAAAAGATAGAAGAACATGGCAACTTAGACTTTCTGGAGCAAATCCATGTCTGGAGAA
TTCCTAGTTCTAAAGTCCATACTGTAAGAGATGAAGAGTGCTCCGAATTATCTATGGTTG
CTGACAAAACAGAAAAGGCTGGTGAATATTCTGTGACGTATGATGGATTCAATACATTACT
ATACCTAACAGACAGACTATGATAACTTCTTATGGCTCACCTCATTAACGAAAAGGATGGGA
AACCTCCAGCTGATGGGCTCTATGCCGAGAACAGATTGAGTTCAGACATCAAGGAAA
GGTTGCACAACATGTGAGGAGCATGGAATCCTAGAGAAAATATCATTGACCTATCCAAT
GCCAACCGCTGCCCTCAGGCCGAGAACATGAGAATGGCCTGAGCCTCCAGTGTGAGTGGAC
ACTTCTCACCAGGACTCCACCATCATCCCTCCTATCCATACAGCATCCCCAGTATAAATT
TGTGATCTGCATTCCATCCTGTCTCACTGAGAAGTCCAATTCCAGTCTATCACACATGTTACC
TAGGATACCTCATCAAGAACATCAAAGACTCTTAAATTCTCTTGATACACCCTGACAAT
TTTCATGAAATTATTCCCTCTGTTCAATAATGATTACCCCTGCACTTAA

FIGURE 174

MKMLLLCLGLTLVCVHAEEASSTGRNFNVEKINGEWTIILASDKREKIEHGNFRLFLEQ
IHVLENSLVLKVHTVRDEECSELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLMAHLI
NEKDGETFQLMGLYGREPDLSSDIKERFAQLCEEHGILRENIIDLMSNANRCLQARE

FIGURE 175

GGCTCGAGCGTTCTGAGCCAGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAA
TGGATTCA~~G~~CCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATA~~CC~~CTTAATTG
TCAGCTTAGTTGAGGAAGACCAATTTC~~T~~CAAAACCCATCTTGCTTGAGTGGTGGTTC
CCAGGAATTATAGGAGCAGGTCTGATGCCATTCCAGCAACAACAATGTCCTGACAGCAAG
AAAAAGAGCGTGCTGCAACAACAGAACTGGAATGTTCTTCATCATTTCAGTGTGATCA
CAGTCATTGGTGCTCTGTATTGCATGCTGATATCCATCCAGGCTCTTAAAAGGTCTCTC
ATGTGTAATTCTCCAAGCAACAGTAATGCCAATTGTAATTTCATTGAAAAACATCAGTGA
CATTCATCCAGAAC~~T~~CAACTGCAGTGGTTTCAATGACTCTTGTGCACCTCCTACTG
GTTCAATAAACCCACCAGTAACGACACCAGGCGAGTGGCTGGAGAGCATCTAGTTCCAC
TTCGATTCTGAAGAAAACAAACATAGGCTTATCCACTTCTCAGTATTAGGTCTATTGCT
TGTTGGAATTCTGGAGGTCTGTTGGCTCAGTCAGATAGTCATCGGTTCCGGCTGTC
TGTGTGGAGTCTAAGCGAAGAAGTCAAATTGTGTAGTTAATGGAAATAAATGTAAGTA
TCAGTAGTTGAAAAAAAAAA

FIGURE 176

MTCCEGWTSCNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMA
IPATTMSLTARKRACCNRTGMFLSSFFSVITVIGALYCMLISIQALLKGPLMCNSPSNSNA
NCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSEENKHRL
IHFSVFLGLLLGVILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

FIGURE 177

GTCGAATCAAATCACTCATTGTGAAAGCTGAGCTCACAGCCGAATAAGCCACC**ATG**AGGCT
GTCAGTGTGTCTCCTGATGGTCTCGCTGGCCCTTGCTGCTACCAGGCCATGCTCTTGCT
GCCAGCTGTTGCTCTGAGATCACAGTCTTATTCTTAAGTGACGCTGCAGTAAACCTC
CAAGTTGCCAAACTTAATCCACCTCCAGAAGCTCTGCAGCCAAGTTGGAAGTGAAGCACTG
CACCGATCAGATATCTTTAAGAACGACTCTCATTGAAAAAGTCCTGGTGGAA**TAG**TGAA
AAAATGTGGTGTGACATGTAAAAATGCTCAACCTGGTTCAAAGTCTTCAACGACACC
CTGATCTTCACTAAAAATTGTAAAGGTTCAACACGTTGCTTAATAAATCACTGCCCTGC

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FIGURE 178

MRLSVCLLMVSLALCCYQAHALVCPAVASEITVFLFLSDAAVNLOVAKLNPPPEALAAKLEV
KHCTDQISFKKRLSLKKSWWK

FIGURE 179

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTGCCAAGGTGACCTCGCAGGACACTGG
TGAAGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTG
GAGCAGATCCGTGGCTGCAGACCCCCGCCCCAGTGCCTCTCCCCCTGCAGCCCTGCCCTC
GAACGTGAC**ATG**GAGAGAGTGACCCCTGGCCCTCTCCTACTGGCAGGCCTGACTGCCTTGG
AAGCCAATGACCCATTGCCAATAAAGACGATCCCTCTACTATGACTGGAAAAACCTGCAG
CTGAGCGGACTGATCTGCGGAGGGCTCCTGCCATTGCTGGATCGCGCAGTTCTGAGTGG
CAAATGCAAATACAAGAGCAGCCAGAACGACAGTCCTGTACCTGAGAAGGCCATCCAC
TCATCACTCCAGGCTCTGCCACTACTTGC**TGA**GCACAGGACTGGCCTCCAGGGATGGCCTGA
AGCCTAACACTGGCCCCCAGCACCTCCTCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTC
TCTCCAAGGGCAGGCTGTTAGGCCCTTCTGATCAGGAGGCTTCTTATGAATTAAACTCG
CCCCACCACCCCCCTCA

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FIGURE 180

MERVTLALLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCK
YKSSQKQHSPVPEKAIPLITPGSATTC

FIGURE 181

GGAGAAGAGGTTGTGGACAAGCTGCCGACAGAAGG**ATG**TGCTGCTGAGCCTGCC
 TGGCTGGGCCTCAGACCGGTGGCAATGTCCCCATGGCTACTCCTGCTGCTGGTTGTGGCTC
 CTGGCTACTCGCCCGCATCCTGGCTTGGACCTATGCCTTCTATAACAACGTGCCGCCGGCTCC
 AGTGTTCACAGCCCCAAACGGAACGGTTGGGTACCTGGCCTGATCACTCCT
 ACAGAGGAGGGCTTGAAGGACTCGACCCAGATGTCGGCCACCTATTCCCAGGGCTTACGGT
 ATGGCTGGGTCCCATCATCCCCTCATCGTTTATGCCACCCTGACACCATCCGGTCTATCA
 CCAATGCCTCAGCTGCCATTGCACCCAAGGATAATCTCTCATCAGGTTCTGAAGCCCTGG
 CTGGGAGAAGGGATACTGCTGAGTGGCGGTGACAAGTGGAGCCGCCACCGTCGGATGCTGAC
 GCCCGCCTCCATTCAACATCCTGAAGTCCTATATAACGATCTTCAACAAGAGTGCAAACA
 TCATGCTTGACAAGTGGCAGCACCTGGCCTCAGAGGGCAGCAGTCGTCGGACATGTTGAG
 CACATCAGCCTCATGACCTTGGACAGTCTACAGAAATGCATCTTCAGCTTGACAGCCATTG
 TCAGGAGAGGCCAGTGAATATATTGCCACCCTTGGAGCTCAGTGCCCTGTAGAGAAAA
 GAAGCCAGCATATCCTCCAGCACATGGACTTCTGTATTACCTCTCCATGACGGCGGCC
 TTCCACAGGGCCTGCCGCCTGGTCATGACTCACAGACGCTGTATCCGGAGCAGGGCGTCG
 CACCCCTCCCCACTCAGGTATTGATGATTTTCAAAGACAAAGCCAAGTCCAAGACTTGG
 ATTTCATTGATGTGCTCTGCTGAGCAAGGATGAAGATGGGAAGGCATTGTCAGATGAGGAT
 ATAAGAGCAGAGGCTGACACCTCATGTTGGAGGCCATGACACCACGGCCAGTGGCCTCTC
 CTGGGTCTGTACAACCTTGCAGGGCACCCAGAATACCAGGAGCGCTGCCACAGGAGGTGC
 AAGAGCTCTGAAGGACCGCGATCTAAAGAGATTGAATGGGACGACCTGGCCAGCTGCC
 TTCCTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCAGCTCCCTCATCTCCG
 ATGCTGCACCCAGGACATTGTTCTCCAGATGGCCAGTCATCCCCAAAGGCATTACCTGCC
 TCATCGATATTATAGGGTCCATCACAAACCAACTGTGTGGCCGGATCTGAGGTCTACGAC
 CCCTCCGCTTGACCCAGAGAACAGCAAGGGAGGTACCTCTGGCTTTATCCTTCTC
 CGCAGGGCCCAGGAACGTGCATGGCAGGGCGTCCGAGATGGGGAGATGAAAGTGGCCTGG
 CGTTGATGCTGCTGCACCTCCGGTCTGCCAGACACACTGAGCCCCGAGGAAGCTGGAA
 TTGATCATGCGCGCCGAGGGCGGGCTTGGCTGCGGGTGGAGCCCTGAATGTAGGCTTGCA
GTGACTTCTGACCCATCCACCTGTTTTGCAGATTGTCATGAATAAACGGTGCTGTCAA

FIGURE 182

MSLLSLPWLGLRPVAMSPLLLLLVGSWLLARILAWTYAFYNNCRLQCFPQPPKRNWFWG
HLGLITPTEEGLKDSTQMSATYSQGFTVWLGPPIIPFIVLCHPDTIRSITNASAAIAPKDNLF
IRFLKPWLGEGISSGGDKWSRHRMLTPAFHFNILKSYITIFNKSANIMLDKWQHLASEGS
SRLDLDFEHISLMTLDSLQKCIFSFDHCQERPSEYIATILELSALVEKRSQHILQHMDFLYY
LSHDGRRFHACRLVHDFTDAVIREERRTLPTQGIDDDFKDKAKSKTLDFIDVLLSKDEDG
KALSDEDIRAEADTFMFGGHDTTASGLSWVLYNLRHPEYQERCRQEVAELLKDRDPKEIEW
DDLAQLPFLTMCVKESLRLHPPAPFISRCCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVW
PDPEVYDPFRFDPENSKGRSPLAFIPFSAGPRNCIGQAFAMAEMKVVLALMLHFRFLPDHT
EPRRKLELIMRAEGGLWLRVEPLNVGLQ

FIGURE 183

CAACAGAAGCCAAGAAGGAAGCCGTATCTTGTGGCGATC**ATG**TATAAGCTGGCCTCCTGC
TGTGGCTTTCACAGGATTCTTAAATCCTCTCTTATCTCTTCCTCTCCTGACTCCAGGGA
AATATCCTTCAACTCTCAGCACCTCATGAAGACGCCGCTTAACCCGGAGGAGCTAGAAA
GAGCTTCCCTTCTACAGATATTGCCAGAGATGCTGGGTGCAGAAAGAGGGGATATTCTCAGG
AAAGCAGACTCAAGTACCAACATTTAACCCAGAGGAAATTGAGAAAGTTCAAGGATT
CTCTGGACAAGATCCTAACATTTACTGAGTCATCTTGCCAGAATCTGGAAACCATA
AGAAACGTGAGACTCCTGATTGCTCTGGAAATACTGTGTC**TGA**AGTGAATAAGCATCTGT
TAGTCAGCTCAGAACACCCATCTAGAATATGAAAAATAACACAATGCTTGATTGAAAAC
AGTGTGGAGAAAATAGGCAAACACACCCCTGTTACCTGGAAAATAATCCTCT
ATGTTTGCACAAAAAAAAAAAAAA

FIGURE 184

MYKLASCCLLFTGFLNPLSLPLLDREISFQLSAPHEARLTPEELERASLLQILPEMLGA
ERGDILRKADSSTNIFNPRGNLRKFQDFSGQDPNILLSHLLARIWKPYKKRET PDCFWKYCV

FIGURE 185

GAACATTTAGTTCCAAGGAATGTACATCAGCCCCACGGAAGCTAGGCCACCTCTGGGAT
GGGGTTGCTGGTTAAAACAAACGCCAGTCATCCTATATAAGGACCTGACAGCCACCAGGCA
CCACCTCCGCCAGGAACTGCAGGCCACCTGTCTGCAACCCAGCTGAGGCCATGCCCTCCCC
AGGGACCGTCTGCAGCCTCCTGCTCGCATGCTCTGGCTGGACTTGGCCATGGCAGGCT
CCAGCTCCTGAGCCCTGAACACCAGAGTCAGCAGAGAAAGGAGTCGAAGAAGCCACCA
GCCAAGCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCGGCCCGGAAGATGGAGGTCAAGCAGA
AGGGGCAGAGGATGAACTGGAAGTCCGGTTAACGCCCCCTTGATGTTGGAATCAAGCTGT
CAGGGGTTCACTTACAGCAGCACAGCCAGGCCCTGGGAAGTTCTTCAGGACATCCTCTGG
GAAGAGGCCAAAGAGGCCAGCCGACAAGTGATCGCCCACAAGCCTACTCACCTCTCT
AAGTTAGAAGCGCTCATCTGGCTTTCGCTTGCTGCAGCAACTCCCACGACTGTTGTA
CAAGCTCAGGAGGCGAATAATGTTCAAACGTGA

FIGURE 186

MPSPGTVCSLLLGMWLIDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPEDG
GQAEGAEDLEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADKO

FIGURE 187

CGGCCACAGCTGGCATGCTCTGCCTGATGCCATCCTGCTGTATGTCCTCGTCCAGTACCTC
 GTGAACCCCAGGGTGCTCCGCACGGACCCAGATGTCAGAAAT**TGA**ACACGTGGCTGCTGT
 TCCTCCCCCTGTTCCCGGTGCAGGTGCAGACCCCTGATAGTCGTGATCATCGGGATGCTCGTG
 CTCCTGCTGGACTTCTTGGCTGGCACCTGGGCCAGCTGCTCATCTTCCACATCTACCT
 GAGTATGTCACCCACCCTAACGCCCCGATCCCCCAAGGCTGGTGGTCAGAGCTGCTCATC
 TTACACCTCTACTTGAGTATGTCCTAACCTGAGCCCCCACGCCTGGGCCAGAGTC
 GTCCCCCGTGTGCGCATGTTCAAGGTCAAGCTCTCCAGAAGTGAGATCATGGACAAAAA
 GGGCAAATCACAGGAAGAAATTAAATCCATGAGGACCCAGCAGGCCAGCAAGAAGCTGAAC
 TCACGCCGAGACCTGCAGGAGTGGTGCCAGGTGCT**TGA**AGTAACAAGTTAAAATGTCAGA
 GACAATGGAATGGAATCTATTAGGAAGAACAGGACATTATGAAATAAGGACAGGTGGACTT
 CCAAAACACAAGTAGAAATTCTAACATGAAATATATTACAGGCAGGTACCCACTAACCA
 AACAACTGAAGCGAGAGCTGTTGCTCACAGTGGCACAGCGGTAGGCAGTC
 AGTCATGTTGCTGAACGACGGAGGGTAAACTCCCCAGCCCCAAGAAAACCTGTGTTGGAAGT
 AACAAACAACCTCCCTGCTCCTGGCACCAAGCCGTTGGTCATGGTGGCCAGCTGCAAAGCG
 TCTTCCATTCTGGGCAGTGGTGGCCCCAGGGCTGTGGCTCTCAGGGGTTCTGTGGAC
 ACGGGCAGCAGAGTGTGTCAGGCCAGCCCCAAGAATGCCCTGCTCCTGACAGCTGGCCA
 ACCCTGGTCAGGGCAGAGGGAGTTGGGTGGCTCAGGCTCTGGCTCACCTCCATCTCCAGA
 GCATCCCCTGCCTGCAGTTGTGGCAAGAACGCCAGCTCAGAATGAACACACCCCCACCAAGA
 GCCTCCTGTTCATAACACACAGGTTACCCCTACAAACCAACTGTCCCCACACAACCCGGGAT
 GTTTAAAACACACACCTCTAACGCATATCTTACAGTCAGTCACTGTTGTCTGCCTGAGGGTTGA
 ATTTTTTTAATGAAAGTGCAATGAAAATCACTGGATTAAATCCTACGGACACAGAGCTGAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 188

MNTWLLFLPLFPVQVQTLLIVVIIGMLVLLDFLGLVHLGQLLIFHIYLSMSPTLSRSPQGW
VVRAAHLTPLLEYVPNPEPPTPGARVFVPRVRMCSGSASPRSEIMDKKGKSQEEIKSMRTQQ
AQQEAEELTPRPAGVVPGA

FIGURE 189

GGAGTGCAGATGGCATCCTCGGTTCTCCAGACAAGCTGCAAGACGCTGACC**ATG**GCCAAG
 ATGGAGCTCTCGAAGGCCTTCTCTGGCCAGCGGACACTCCTATCTGCCATCCTCAGCATGCT
 ATCACTCAGCTTCTCCACAACATCCCTGCTCAGCAACTACTGGTTGGGCACACAGAAGG
 TGCCCAAGCCCCGTGCGAGAAAGGTCTGGCAGCCAAGTGCTTGACATGCCAGTGTCCCTG
 GATGGAGATAACCAACACATCCACCCAGGAGGTGGTACAATACAACACTGGGAGACTGGGATGA
 CCGGTTCTCCTCCGGAGCTCCGGAGTGGCATGTGGCTATCCTGTGAGGAAACTGTGGAAG
 AACCAGGGGAGAGGTGCCGAAGTTCATTGAACCTACACCACAGCCAAGAGAGGGTGAGAAA
 GGACTACTGGAATTGCCACGTTGCAAGGCCATGTCACCCACTCTCCGATTGGAGGGAA
 GC GGTTGATGGAGAAGGCTCCCTCCCCTCCCTCCCTGGGGCTTGTGGCAAAATCCTA
 TGGTTATCCCTGGGAACGCAGATCACCTACATCGGACTTCAATTCATCAGCTTCCTCCTGCT
 ACTAACAGACTTGCTACTCACTGGAACCCCTGCCTGTGGCTCAAACGTAGCGCCTTGCTG
 CTGTTCCCTCTGTCCTGTCAGGTCTCCTGGGGATGGTGGCCACATGATGTATTACAAGTC
 TTCCAAGCGACTGTCAACTGGTCCAGAAGACTGGAGACCACATGTTGGAATTATGGCTG
 GGCCTTCTACATGGCCTGGCTCCTCACCTGCTGCATGGCGTCGGCTGTCACCACCTCA
 ACACGTACACCAGGATGGTGGCTGGAGTTCAAGTGCAAG**CATAG**TAAAGAGCTCAAGGAAAAC
 CCGAACTGCCTACCACATCACCACAGTGTTCCTCGCGGCTGTCAAGTGCAAGCCCCAC
 CGTGGGTCTTGACCAGCTACCACCACTATCATAATCAGCCCACCTCTGTCTGAGG
 GAGTCGACTTCACTCCGAGCTGCGGAACAAGGGATTCAAAGAGGGCCAGCCAGGAGCTG
 AAAGAACGAGTTAGGTCACTGTAGAGGAAGAGCAGTGTAGGAGTTAACGGGTTGGGA
 GTAGGCTTGAGCCCTACCTTACACGTCTGCTGATTATCAACATGTGCTTAAGCCAACATCCG
 TCTCTGAGCATGGTTTAGAGGCTACGAATAAGGCTATGAATAAGGGTTATCTTAAGTC
 CTAAGGGATTCTGGGTGCCACTGCTCTCTTCTACAGCTCCATCTGTGTTACCCAC
 CCCACATCTCACACATCCAGAATTCCCTCTTACTGATAGTTCTGTGCCAGGTTCTGGC
 TAAACCATGGAGATAAAAAGAAGAGTAAAATACACTTCCCCGACCTTAAGGATCTGAAA

FIGURE 190

MAKMELSKAFSGQRTLLSAILSMILSLSFSTSLLSNYWFVGTQKVPKPLCEKGLAAKCFDMP
VSLDGDTNTSTQEVVQYNWETGDDRFSFRSFRSGMWLSCEETVEEPGERCRSFILETPPAKR
GEKGLLEFATLQGPCHPTLRFGGKRLMEKASLPSPPLGLCGKNPMVIPGNADHLHRTSIHQL
PPATNRLATHWEPCWAQTERLCCFLCPVRSPGDGGPHDVFTSLPSDCQLGSRRLETTCLE
LWLGLLHGLALLHLLHGVGCHHLQHVHQDGAGVQVA

FIGURE 191

AACTGGAAGGAAAGAAAGAAAGGTCA GCTTGGCCAG **ATGTGGTTACCCCTGGTCTCCTG**
TCTTTATGTCTTCTCCTCTTCCTATTCTGCATCTCCCTCACTTAAGTCTCAGGCCTGTCA
GCAGCTCCTGTGGACATTGCCATCCCTCTGGTAGCCTCAGAGCAAACAGGACAACCTATG
TTATGGATGTTCCACCAACCAGGGTAGTGGCATGGAGCACCGTAACCCTGTGCTCTGT
GATCTCTATGACAGAGCCACTTCTCCACCTCTGAAATGTTCCCTGCTCTGAAATCTGGCATG
AGATGGCACAGGTGACCACGCAGAAGCCACCAGAACATCTGCCTGCCCTATTCCCTCCCAA
GTCTGTTCTTATTGTCAACCTCAGCACAACAGGCTGGGCCAATGGCATTACAGAGAAAG
CAATCTGTGTGGCTAGTGGCAGATTACCATGCAAGCCCCAGGAGAAATGGAGGGCTTGT
AGCCACCTCCCTGTCAGCCAGTATTAACATGTCCTCCCTGCCCGCCGTAGATTCA
GACATTGCCCTGTGTGCCACCAAACCAAGGACTTCCAGGGCAGTGTAGCATTTCAAGCTCCGTACT
CTCCTGGTACCCAGCAAGACGTCTGTTCCAGGGCAGTGTAGCATTTCAAGCTCCGTACT
ATGGCGATGGCCATGATGTTACAATCCCAC TGCCCTGAATAATCAAGTGGGAAGGGGAAGCA
GAGGGAAATGGGGCCATGTGAATGCAGCTGCTGTTCTCCCTACCCCTGAGGAAAAACCAA
GGGAAGCAACAGGAACCTCTGCAACTGGTTTTATCGAAAGATCATCCTGCCGTGAGATGC
TGTTGAAGGGGCACAAGAAATGTAGCTGGAGAAGATTGATGAAAGTGCAGGTGTAAAGGAA
ATAGAACAGTCTGCTGGGAGTCAGACCTGGAATTCTGATTCAAACCTTTATTACTTGGG
AAGTCACTCAGCCTCCCCGTAGCCATCTCAGGGTGACGGAACCCAGTGTATTACCTGCTGG
AACCAAGGAAACTAACAAATGTAGTTACTAGTGAATACCCCAATGGTTCTCCAATTATGCC
CATGCCACCAAAACAATAAAACAAAATTCTCTAACACTGAAA

FIGURE 192

MWLPLGLLSSLCLSPLPILSSPSLKSQACQQLLWTLPSPLVAFRANRTTYVMDVSTNQGSGME
HRNHLCFCDLYDRATSPPPLKCSLL

FIGURE 193

GTAGCGCGTCTGGGTCTCCGGCTGCCGCTGCTGCCGCCCTCGGTGAGGCAGGAGCAGTCA
 CCGCC**ATG**GCAGGCATCAAAGCTTGATTAGTTGCTTGGAGGAGCAATCGGACTGATGTTTGATGCTT
 GGATGTGCCCTCCAATATAACAAATACTGGCCCTTGTCTATTGTTACATCCTTCACCTATTCC
 ATACTGCATAGCAAGAAGATTAGTGGATGATAACAGATGCTATGAGTAACGCTTGTAAAGGAAC
 TTACAACGGGCATTGCGTGTAGCTTGGACTCCCTATTGTTGCAAGAGCACATCTGATTGAGTGGG
 GCTTGTGCACCTGTCACAGGAAACACAGTCATCTTGCACACTATACTAGGCTTTCTTGGTCTTGAAG
 CAATGACGACTTCAGCTGGCAGCAGTGG**TGA**AAAGAAATTACTGAACATTGTCAAATGGACTCTGTCATTT
 GTTGGCCATTCAACGACACAGGAGATGGGGAGTTAATGCTGAATGGTATAGCAAGCCTTGGGGTATT
 GGTGCTCCCTCTCACTTTATTGTAAGCATACTATTTCACAGAGACTGCTGAAGGATAAAAGGATTTCT
 CTTTGAAAGCTGACTGATTTACACTATCTAGTATGCTTTGGTGTCTGCTGAATTAAATAT
 TTATGTTTTCTGTTAGGTTGATTGAAATCAATATGCAATGTTAAACACTTTTAATGTAATCA
 TTTGCATTGGTAGGAATTACAATTCCGCCGGCTCTATTACTGGTCAAGTACATCTTCTTAAATTATT
 TAGCCTCCATTATTACAAAAAAATTATAAAATAAGTTTCAGTCAGTCAGGATGACATCACTCCAAATG
 CAGACATACAGACGGTGGCATACGTTAGACTGTATACTGCAAAATATAGCTGCATTACCTCAGAG
 GGGCCAAGTGTAAATGCCATGCCCTCCGTTAAGGGTTGGTTACTGGTAGACAGATGTTGGGATTG
 AAAATTATTATGAAATTGCTACAGAGGAGTGCTTCTCTCAATTGTTAGAAGAATTATGTTAAACTTA
 AGGTAAAGGGTGTAAAAACATTGAGATAAGGTTTTATTGTTATTGTTAGAGTGAGTTGCAATGT
 GGGAAAGAAATGACATTGAAATTCCAGTTGGTAACTCTGTTCTATTATAAGTGAATTGTTGATCTCT
 AACCTTCATGTTTACCCCTGTTAAAGAACATACATGAAACCACACTGATGAGGGACAGTGTATGTTG
 ATCATATATGCCAGAAAACCTCCTCTGCTCCTCTTGAATTGTTATGTTGATATATTACATAAAA
 TAACTTCAAATATACTGTTAAACACTAGAAGTGTACTTACCTGAAAATAATTGCTATGCCGTACATT
 CAGAGTCCCCCTCCCTGCAAGGCCTTGCATGATTAACAAGTAACCTGTTAGTCTTACAGATAATTG
 TTAACAGTTAAAGATTAGACCATGGTAAAGTAGTTCTTATCTCAAGGTTATATCATATGTAATTAAAG
 TATTGTTAAGACAAGTTCTGTATACCTCTGAACCTGTTGATTGAGTTCATCATGATAGATCTG
 CCTTATAAAAGGCATTGTTGTGAGTAATGCAAAGTAGCCAAGTCCAGCTATATAGCAGCTCAGAAACAT
 ACCTGACCAAAAAATTCCCAGTAACCAGGCATGATCAATTATAGTGGCGTTACATCTAATAATTACAGGA
 CTTTTTCAGGAGTGGTTATAAAACATTCAAGTTGGTCTGACAGTATTGTTAAGGATATTGTTGATG
 TTTATTCACTTACATAAAATTATTGCGCATCAGCCAAACTCAGTAATCATGACAGCTGCTGTTG
 TTTATGAAAGTTATTCTCAAGAAATGGAATAATTGGGATTGTTAGCTTACAAAGATGCC
 AGCCACAGGTTTATTGCTAAAGGCATGACTTTAGATATGAGATGACGGGAAGCAGGACGAAATATCG
 GCGTGTGGCTGGAGCCTCCACTGGAGGCTGAAAGTGGCTTGTGGTATTATAATGTCAGATTCAAGGG
 GGTGCAGGTACACATGAGTTAGAGAGCTGGTGGAGACAGTGGAAACTCTTGTGCTGTGATCTACTGG
 TTTTTGCGAGGAAGTGCATTCTCTGGTCTTCCATTGTTCTGATGTCAGTGCAGTGCAGTGC
 TTTTATCCACTTGGCCACAGACTTTCTAACAGCTGGTATTATTCTATATACTAATTGCAATTGG
 CAGGCTAGTTGAGATGACATAGCTGCTGCTCTGATTCTAGGCTAGTTACTTGAGATGAA
 TTTCCATAGAATATGCACTGATAACACATTCTATGGAAAGAAAATTGATGATGAAACAATAA
 AGATTAAATATCTATTAAAAAA

FIGURE 194

MAGIKALISLSFGGAIGLMFLMLGCALPIYNKYWPLFVLFFYILSPIPYCIARRLVDDTDAM
SNACKELAIFLTGIVVSAFGLPIVFARAHLIEWGACALVLTGNTVIFATILGFFLVFGSND
DFSWQQW

FIGURE 195

FIGURE 196

MDFLLLGLCLYWLLRRPSGVVLCLLGACFQMLPAAPSGCPQLCRCEGRLLYCEALNLTEAPH
NLSGLLGLSLRYNSLSELРАGQFTGLMQLTWLYLDHNHICSVQGDAFQKLRRVKELTLSSNQ
ITQLPNTTFRPMPNLRSDLSYNKLOALAPDLFHGLRKLTTLHMRANAIQFVPRIFQDCRS
LKFLDIGYNQLKSLARNSFAGLFKLTELHLEHNDLVKVNFAHFPRLISLHSLCLRRNKVAIV
VSSLWDWNLEKMDLSGNEIEYMEPHVFETVPHLQLDSLRLTYIEPRILNSWKS LTSIT
LAGNLWDCGRNVCALASWLSNFQGRYDGNILQCASPEYAQGEDVLDavyAFHLCEDGAEPTSG
HLLSAVTNRSDLGPASSATTLADGGEQHDGTFEPATVALPGGEHAENAVQIHKVVTGTMA
LIFSFLIVVLVLYVSWKCFPASLRQLRQCFTQRRKQKQKQTMHQMAAMSAQEYYVDYKPNH
IEGALVIINEYGSCCTCHQQPARECEV

FIGURE 197

GTGCAAGGAGCCGAGGCAGATGGCGTCTGGCCGGTCTGCTGGCTGCAGCTCTGC
GCACTGACCCAGGCGGTCTCCAAACTCTGGGTCCCCAACACGGACTTCGACGTGCAGCAA
CTGGAGCCAGAACGGACCCGTGCGCCGGCGGCCGTTGAGTTCCCGGGACAAGATGG
TGTCAGTCCTGGTGAAGAAGGTACGCCGTCTCAGACATGCTCCTGCCGCTGGATGGGAA
CTCGTCTGGCTTCAGGAGCCGGATTGGCGTCTCAGACGTGGCTCGCACCTGGACTGTGG
CGCGGGCGAACCTGCCGTCTCCCGACTCTGACCGCTCTCCTGGCATGACCCGACCTGT
GGCGCTCTGGGGACGAGGCACCTGGCCTCTCGTGGACGCCGAGCGCGTGCCCTGCCGC
CACGACGACGTCTTCCGCCTAGTGCCTCCTCCCGTGGGCTCGGCCCTGGCGCTAG
CCCCGTGCGTGTCCGCAGCATCTGGCTCTGGCCGGACGTTCACGCGACGAGGACCTGG
CTGTTTCCTGGCGTCCCGCGGGCCGCCTACGCTTCCACGGGCCGGCGCCTTGACGGTG
GGCCCCGAGGACTGCGCGAACCGTGGCTCGTCTGGCAACGCGGAGGCGCAGCCGTG
GATCTGCGCGGCCCTGCTCCAGCCCC

FIGURE 198

MGVLGRVLLWLQLCALTQAVSKLWVPNTDFVAANWSQNRTPCAGGAVEFPADKMSVLVQE
GHAVSDMLLPLDGEVLASGAGFGVSDVGSHLDCGAGEPAVFRDSDRFSWHDPHLWRSGDEA
PGLFFVDAERVPCRHDDVFFPPSASFRVGLGP GAS PVRVRSISALGRTFTRDEDLAVFLASR
AGRLRFHGP GALSVG PEDCADPSGC VCGNAEAQPWICA ALLQP

FIGURE 199

ATCGCATCAATTGGGAGTACCATCTTCCTC**ATG**GGACCAGTGAAACAGCTGAAGCGAATGTT
TGAGCCTACTCGTTGATTGCAACTATCATGGTGCTGTTGTGTTGCACTTACCCGTGTT
CTGCCTTTGGTGGCATAACAAGGGACTTGCACTTATCTTCTGCATTGAGCTTTGGCA
TTGACGTGGTACAGCCTTCCTCATACCATTGCAAGGGATGCTGTGAAGAAGTGTGTTGC
CGTGTGTCTGCA**TAATT**CATGGCCAGTTTATGAAGCCTTGGAAGGCACTATGGACAGAAC
CTGGTGGACAGTTTGTAACTATCTCGAACCTCTGTCTACAGACATGTGCCTTTATCT
TGCAGCAATGTGTTGCTTGATTGACACATTGAGGGTTACTTTGAGCAACAATACAT
TCTCGAACCTGAATGTCAGTAGCACAGGATGAGAAGTGGTTCTGTATCTTGTGGAGTGGAA
TCTTCCTCATGTACCTGTTCTCTGGATGTTGCCCCACTGAATTCCCATGAATAAAC
CTATTCAACAGCAA
AAAAAAAAAAAAAAAAAAAAAA

200/330

FIGURE 200

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCASFWWNKGLALIFCILQSLALTWYSLSFIP
FARDAVKKCFAVCLA

FIGURE 201

TTGAGCGCAGGTGAGCTCCTGCGGTTCCGGGGCGTTCCTCCAGTCACCCCTCCGCCGTTACCCGCCGCG
 CCGAGGGAGTCTCCTCCAGACCCCTCCCTCCGTTGCTCAAACATAATACGACTGAACGGATCGTGCAGGGT
 GGGAGAGAAAATTAGGGGGAGAAGGACAGAGAGAGCAACTACCATCCATAGCCAGATAGATTATCTTACACTG
 AACTGATCAAGTACTTGAAA**ATG**ACTTCGAAATTATCTTGGTGTCTCATACTTGCTGCACTGAGTCTTC
 AACCACCTTCTCCAAGTAGACCAGCAAAAGGTTCTACTAGTTCTTGTGATGGATTCCGTTGGGATTACT
 TATATAAAGTCCAAGCCCCATTTCATTATATTATGAAATATGGTGTCTGAGCAAGTTACTAATGTT
 TTTATTACAAAACCTACCCCTAACCAATTATCTTGGTAACTGGCCTCTTGAGAGAATCATGGGATTGTTGC
 AAATGATATGTTGATCCTATCGGAACAAATCTTCTCCTGGATCACATGAATATTATGATTCCAAGTTT
 GGGAGAAGCGACACCAATATGGATCACAAACAGAGGGCAGGACATACTAGTGGTGCAGCCATGTGGCCCGA
 ACAGATGAAAAATACATAAGCGTTCTACTCATTACATGCCCTAACATGAGTCAGTTCTATTGAAGATAG
 AGTTGCCAAAATTGTAATGGTTACGTCAAAAGAGCCCATAAATCTGGTCTTCTATTGGAAAGACCC
 ATGACATGGGCCACCTTGGGACCTGACAGTCGCTCATGGGGCCTGTCATTCAAGATATTGACAAGAAGTTA
 GGATATCTCATACAAATGCTGAAAAGGCAAGTTGTGGAACACTCTGAACCTAACATCACAGTGATCATGG
 AATGACCGAGTGTCTGAGGAAAGGTTAATAGAACTTGACAGTACCTGGATAAAGACCACTAACCTGATTG
 ATCAATCTCCAGTAGCAGCCATCTGCCAAAAGAAGGTAATTGATGAAGTCTATGAAGCACTAACCTACGCT
 CATCCTAATCTTACTGTTACAAAAAGAACGAGCTCCAGAAAGGTGGCATTACAATACACAGTCGAATTCA
 ACCAATCATAGCAGTGGCTGATGAAGGGTGGCACATTACAGAATAAGTCAGATGACTTCTGTTAGGCAACC
 ACGGTTACGATAATGCGTAGCAGATATGCATCCAATATTTAGCCATGGCCTGCCTCAGAAAGAATTTC
 TCAAAAGAAGCCATGAACCTCACAGATTGTACCCACTACTATGCCACCTCCTCAATATCACTGCCATGCCACA
 CAATGGATCATTCTGAATGTCCAGGATCTGCTCAATTCAAGCAATGCCAAGGGTGGCCCTTACACAGAGTA
 CTATACTCCTCCCTGGTAGTGTAAACCGACAGAATATGACCAAGAGGGTCAACCTTATTTCATAGGGTC
 TCTCTGGCAGCATTAGTGTATTGTAATTTCATTAAGCAATTACAGTCAGTCAAATACCTGC
 CTTACAAGATATGCATGCTGAAATAGCTAACCATATTACAAG**CC****TAATGTTACTTGAAAGTGGATTG**CATA
 TTGAAGTGGAGATTCATAATTATGTCAGTGTAAAGGTTCAAATTCTGGAAACCAGTTCAAACATCTGC
 AGAAACCATTAAGCAGTTACATATTAGGTATACACACACACACACACACACACACACGGACCAAA
 ATACTTACACCTGCAAAGGAATAAAGATGTGAGAGTATGTCCTCATTGTCACTGTAGCATAGGGATAGATAAG
 ATCCTGCTTATTGGACTTGGCGCAGATAATGTATATTAGCAACTTGCACTATGTAAGTACCTTATAT
 ATTGCACCTTAAATTCTCTCTGATGGGTACTTTAATTGAAATGCACTTGTGATTGAGTTATGTCTTATAAC
 TTGATTGAAATGACAACCTTTGCACCCATGTCAGAATACTTGTACGCAATTGTCAGTCAAACACTGAAGGAAATT
 TCTAATAATCCGAATAATGAACATAGAAATCTATCCATAAAATTGAGAGAAGAAGGATGATAAGTGTGA
 AAATTAATGTGATAACCTTGAACCTTGAATTGGAGATGATTCCAAACAGCAGAATGCAACTGTGGCAG
 TTCTGCTTATTCTTCCAGAGAACGTTGTTCTATTATTTCCCTCAAAAGAGAGTCAAACTGACAG
 ATTGTTCTAAATATATTGTTCTGTCATAAAATTATTGATTTCTGATGAGTCATATTACTGTGATTTC
 TAATAATGAAGACACCATGAATATACCTTCTTCTATATAGTCAGCAATGGCCTGAATAGAAGCAACCAGCA
 CCATCTCAGCAATGTTCTCTGTTGTAATTATTGCTCCTTGAATTAAATCACTATTACATTAA
 AAATCAAATTGGATAAAAAAAAAAAAAAA

09998845551111115555

FIGURE 202

MTSKFILVSFILAALSLSTTFSQLDQQKVLLVSDGFRWDYLYKVPTPHFYIMKYGVHVK
QVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFLDHMNIYDSKFWEETPIW
ITNQRAGHTSGAAMWPGBTDKIHKRFPTHMPYNESVSFEDRVAKIVEWFTSKEPINLGLLY
WEDPDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIITSDHGMTQCSEER
LIELDQYLDKDHYTLIDQSPVAAILPKEGKFDEVYEALTHAHPNLTVYKKEDVPERWHYKYN
SRIQPIIAVADEGWHILQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFRKNFSKEAMNSTD
LYPLLCHLLNITAMPHNGSFVNQDLLNSAMPRVVPTQSTILLPGSVKPAEYDQEGSYPYF
IGVSLGSIIVIVFFVIFIKHЛИHSQIPALQDMHAEIAQPLLQA

Signal Peptide:

amino acids 1-22

Transmembrane Domain:

amino acids 429-452

N-glycosylation sites:

amino acids 101-104, 158-161, 292-295, 329-332, 362-365, 369-
372, 382-385, 389-392

Somatomedin B Domain:

amino acids 69-85

Sulfatase protein Region:

amino acids 212-241

FIGURE 203

GGATTTGTGATCCCGATTGCTCCCACGGCGGGACCTTGTAAGTCGGGAGGCCAG
 GACAGGCCACCCTGCAGGGCGGGAGGCAGCCGGGTGAGGGAGGTGAAGAAACCAAGACGC
 AGAGAGGCCAACGCCCTGCCTGGTACACAGCAAAGGAGGCAGAGCCAGAACTCACAA
 CCAGATCCAGAGGAACAGGGAC**ATG**GCCACCTGGGACAAAAGGCAGTCACCCGCAGGGC
 AAGGTGGCTCCCGCTGAGAGGATGAGCAAGTTCTAAGGCACCTCACGGTCGTGGAGACGA
 CTACCATGCCTGGAACATCAACTACAAGAAATGGGAGAATGAAGAGGAGGAGGAGGAGG
 AGCAGCCACCACCCACACCAGTCTCAGGCAGGAAGGCAGAGCTGCAGCCCTGACGTTGCC
 CCTGCCCTGGCCCCGCACCCAGGGCCCCCTGACTTCAGGGCATGTTGAGGAAACTGTT
 CAGCTCCCACAGGTTTCAGGTACATCATCATCTGCTTGGTGGTCTGGATGCCCTGGTGC
 TTGCTGAGCTCATCCTGGACCTGAAGATCATCCAGCCGACAAGAATAACTATGCTGCCATG
 GTATTCCACTACATGAGCATCACCACATTGGTCTTTTATGATGGAGATCATTTAAATT
 ATTTGCTTCCGCCTGAGTTCTTACCAAGTTGAGATCCTGGATGCCGTGGTGG
 TGGTCTCATTCATCCTGGACATTGTCCTCTGTTCCAGGAGCACCAGTTGAGGCTCTGGC
 CTGCTGATTCTGCTCCGGCTGTGGCGGGTGGCCCGGATCATCAATGGGATTATCATCTCAGT
 TAAGACACGTTAGAACCGCAACTCTTAAGTTAAAACAGATGAATGTACAATTGGCCGCCA
 AGATTCAACACCTTGAGTTAGCTGCTCTGAGAAGCCCTGGAC**TGAT**GAGTTGCTGTATC
 AACCTGTAAGGAGAAGCTCTCCGGATGGCTATGGAATGAAAGAATCCGACTTCTACTCT
 CACACAGCCACCGTGAAAGTCCTGGAGTAAAATGTGCTGTGTACAGAAGAGAGAGAAGGAAG
 CAGGCTGGCATGTTCACTGGGCTGGTGTACGACAGAGAACCTGACAGTCAGTGGCCAGTTA
 TCACATTCAAGATTACAAATCACACAGAGCATCTGCCTGTTCAATCACAAGAGAACAAACC
 AAAATCTATAAAGATATTCTGAAAATATGACAGAATTGACAAATAAAGCATAACGTGTA
 AAAAAAAAAAAAAAAAAAAAAAA

FIGURE 204

MATWDEKAVTRRAKVAPAERMSKFLRHFTVVGDDYHAWNINYKKWENEAAAAAQQPPPTPV
SGEEGRAAAPDVAPAPGPAPRAPLDFRGMLRKLFFSHRFQVIIICLVVLDALLVLAELILDL
KIIQPDKNNYAAMVFHYMSITILVFFMMEIIFKLFVFRLSSFTSLRSWMPVVVVVSFILDI
VLLFQEHQFEALGLLILLRLWRVARIINGIIISVKTRSERQLRLKQMNVQLAQKIQHLEFS
CSEKPLD

FIGURE 205

CGGCTCGAGCTGAGCCGAATCGGCTCGAGGGGCAGTGGAGCACCCAGCAGGCCGCCAAC**AT**
GCTCTGTCTGTGCCTGTACGTGCCGGTCATCGGGGAAGGCCAGACCGAGTTCCAGTACTTTG
 AGTCGAAGGGGCTCCCTGCCAGCTGAAGTCCATTTCAGCTCAGTGTCTTCATCCCCCTCC
 CAGGAATTCTCACCTACCGCCAGTGGAAAGCAGAAAATTGTACAAGCTGGAGATAAGGACCT
 TGATGGCAGCTAGACTTGAAGAATTGTCCATTATCTCCAAGATCATGAGAAGAAGCTGA
 GGCTGGTGTAAAGATTGGACAAAAAGAATGATGGACGCATTGACGCCAGGAGATCATG
 CAGTCCCTGCCGGACTTGGGAGTCAAGATATCTGAACAGCAGGCCAGAAAAATTCTCAAGAG
 CATGGATAAAAACGGCACGATGACCATCGACTGGAACGAGTGAGAGAGACTACCACCTCC
 ACCCGTGGAAAACATCCCCGAGATCATCCTACTGGAAGCATTCCACGATCTTGATGTG
 GGTGAGAATCTAACGGTCCCGATGAGTTCACAGTGGAGGAGAGGAGACGGGATGTGGT
 GAGACACCTGGTGGCAGGAGGTGGGGCAGGGGCGTATCCAGAACCTGCACGGCCCCCTGG
 ACAGGCTCAAGGTGCTCATGCAGGTCCATGCCCTCCCGCAGCAACAAACATGGGATCGTTGGT
 GGCTTCACTCAGATGATTGAGAAGGAGGGCCAGGTCACTCTGGCAGGAGGATCCGGCAGAGAGGGG
 CGTCTCAAATTGCCCGAATGCCATCAAATTCTAGGCCCTATGAGCAGATCAAGGCC
 TTGTTGGTAGTGACCAGGAGACTGAGGATTCAAGAGAGGCTTGTGGCAGGGCTCTGGCA
 GGGGCCATGCCAGAGCAGCATACCCAAATGGAGGTCTGAAGACCCGGATGGCGCTGCG
 GAAGACAGGCCAGTACTAGGAATGCTGGACTGCGCAGGAGGATCCGGCAGAGAGAGGGG
 TGGCCGCTTCTACAAAGGCTATGCCCCAACATGCTGGCATCATCCCCTATGCCGCCATC
 GACCTGCACTACGAGACGCTAAGAATGCCCTGGCTGCAGCAGTACAGTGAACAGCGC
 GGACCCCGCGTGGCTCTGGCCTGTGGCAGCATGTCCAGTACCTGTGGCCAGCTGG
 CCAGCTACCCCTGCCCTAGTCAGGACCCGGATGAGGCCAGGAGGATCCGGCAGAGAGGG
 CCGGAGGTGACCATGAGCAGGCCCTTCAAACATATCTGCAGGACCGAGGGGGCCTCGGGCT
 GTACAGGGGGCTGGCCCCAACATTCTAGAAGGTCTCCAGCTGTGAGCAGTACGTGG
 TCTACAGAGAACCTGAAGATCACCTGGCGTGCAGTCGG**TGA**CGGGGGAGGGCCGCC
 GCAGTGGACTCGCTGATCCTGGCGCAGCCTGGGCTGTGAGCCATCTCATTCTGTGAATG
 TGCCAAACACTAAGCTGTCAGGCCAGCTGTGAAAACCCCTAGACGCACCCGAGGGAGGG
 GGGGAGAGCTGGCAGGCCAGGGCTGTCTGCTGACCCCAGCAGACCCCTCTGTTGGTCC
 AGCGAAGACCACAGGCATTCTTAGGGTCAGGGTCAAGCAGGCTCCGGGCTACATGTGAA
 GGACAGGACATTCTGCAGTGCCTGCCAATAGTGAGCTTGAGCCTGGAGGCAGGCTTAGT
 TCTTCCATTTCACCCCTGCAAGCCAGCTGTGGCCACGGCCCTGCCCTCTGGCTGCCGTG
 ATCTCCCTGTGCCCTTGTGCTGCCCTGTGAGGTAAAGGTGGAGGAGGGCTACAG
 CCCACATCCCACCCCTCGTCCAAATCCATAATCCATGATGAAAGGTGAGGTACGTGGCCT
 CCCAGGCCACTTCCAAACCTACAGCATGACGCCACTTGGCTGTGAGGAAAGAGGAAAG
 GATCTGGCCTTGTGGTCACTGGCATCTGAGCCCTGCTGATGGCTGGGCTCTGGGCTAGCT
 TGGGAGTGCAGGGGGCTCGGGCTGCCCTGGCTGACAGAAGGCAAGTGTGGGGCTCA
 TGGTGCCTGAGCTGGCCTGGACCCCTGTCAGGATGGCCCCACCTCAGAACCAAACACT
 TCCCCACTGTGGCATGAGGGCAGTGGAGCACCATGTTGAGGGCGAAGGGCAGAGCGTTGT
 GTGTTCTGGGGAGGGAAAGGAAAGGTGTTGGAGGCCTTAATTATGGACTGTTGGAAAAGGG
 TTTTGTCCAGAAGGACAAGCCGGACAAATGAGCGACTCTGTGCTTCAGAGGAAGACGAGG
 GAGCAGGAGCTGGCTGACTGCTCAGAGTCTGTTCTGACGCCCTGGGGGTTCTGTCAACC
 CCAGCAGGGGCCAGCAGGCCAGGCCACATTCCACTTGTGTCAGTGTGGTACCTTCCC
 GCTTGTCACTTCAAGTCATTTCATTTCATATTATGTTCTGTTGATGGTGTACCTTCCC
 AAGCCCGCCAGTGGGATGGGAGGAGGAGGAGAAGGGGGCTTGGCCGCTGAGGTGG
 CTGTCAGAGAAATTCTTTGGGACTGGAGGAGAGAAAAGCGGCCAGAAGGCAGCAGCCCTG
 GCTCCTTCTTGGCAGGTTGGGGAGGGCTGCCCTGGCCAGCTTAGGATTCAGGGTTGA
 CTGGGGCGTGGAGAGAGAGGGAGGAACCTCAATAACCTTGAGGTTGAATCCAGTTATT
 CTGCGCTGCGAGGGTTCTTATTCACTCTTCTGAATGTCAAGGCAGTGAGGTGCCTCT
 CACTGTGAATTGTGGGGCGGGGCTGGAGGAGAGGGTGGGGGCTGGCTCCGTCCCTCC
 CAGCCTCTGCTGCCCTGCTTAACAATGCCGCCACTGGCGACCTCACGGTGTGCACTTCC
 ATTCCACCAGAATGACCTGATGAGGAATCTCAATAGGATGCAAAGATCAATGAAAAAATT
 GTTATATATGAACATATAACTGGAGTCGTCAAAAAGCAAATTAAAGAAGAATTGGACGTTAG
 AAGTTGTCAATTAAAGCAGCCTCTAATAAAAGTTCAAAGCTGAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAA

FIGURE 206

MLCLCLYVPVIGEAQTEFQYFESKGLPAELKSIFKLSVFIPSQEFTSYRQWKQKIVQAGDKD
LDGQLDFEEFVHYLQDHKKLRLVFKILDKKNDGRIDAQEIMQSLRDILGVKISEQQAEKILK
SMDKNGMTMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTVPDEFTVEERQTGMW
WRHLVAGGGAGAVSRTCTAPLDRLKVLMQVHASRSNNMGIVGGFTQMIREGGARSLWRNGNI
NVLKIAPESAIKFMAYEQIKRLVGSDQETLRIHERLVAGSLAGAIAQSSIYPMEVLKTRMAL
RKTGQYSGMLDCARRILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLNAWLQHYAVNS
ADPGVFVLLACGTMSSTCGQLASYPLALVRTRMQAQASIEGAPEVTMSSLFKHILRTEGAFG
LYRGLAPNFMKVIPAVSISYVVYENLKITILGVQSR

Important features:

Signal peptide:

amino acids 1-16

Transmembrane domain:

amino acids 284-304, 339-360, 376-394

Mitochondrial energy transfer proteins signature.

amino acids 206-215, 300-309

N-glycosylation site.

amino acids 129-133, 169-173

Elongation Factor-hand calcium-binding protein.

amino acids 54-73, 85-104, 121-140

FIGURE 207

GGAAGGCAGCGGAGCTCCACTCAGCCAGTACCCAGATA CGCTGGAACCTCCCCAGCC**AT**
GGCTTCCTGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAG
 CAATTGCACTCATCATTGGCTTGTTGGTATTCAGGGAGACACTCCATCACAGTCACTACTGTC
 GCCTCAGCTGGAACATTGGGAGGATGGAATCCTGAGCTGCACCTTGAAACCTGACATCAA
 ACTTCTGATATCGTGTACAATGGCTGAAGGAAGGTGTTAGGCTTGGTCCATGAGTTCA
 AAGAAGGCAAAGATGAGCTGTCGGAGCAGGATGAAATGTTAGGCCGGACAGCAGTGT
 GCTGATCAAGTGTAGTTGGCAATGCCCTTTGCGGCTGAAAAACGTGCAACTCACAGATGC
 TGGCACCTACAAATGTTATCATCACTCTAAAGGCAAGGGAAATGCTAACCTTGAGTATA
 AAACTGGAGCCTTCAGCATGCCGAAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTG
 CGGTGTGAGGCTCCCCGATGGTCCCCCAGCCCACAGTGGCTGGCATCCAAAGTTGACCA
 GGGAGCCAACCTCTCGGAAGTCTCCAATACCAGCTTGAGCTGAACCTGAGAATGTGACCA
 TGAAGGTTGTGTCTGTGCTCTACAATGTTACGATCAACAAACACATACTCCTGTATGATTGAA
 AATGACATTGCCAAAGCAACAGGGATATCAAAGTGACAGAACATCGGAGATCAAAAGGCGGAG
 TCACCTACAGCTGCTAAACTCAAAGGCTCTGTGTCTTCTTGTGAACTCAGCT
 GGGCACTTCTGCCCTCAGCCCTACCTGATGCTAAAAT**TAA**TGTGCCTGGCACAAAAAAG
 CATGCAAAGTCATTGTTACAACAGGGATCTACAGAACTATTCACTGAGCTGAGATATGACCTAG
 TTTTATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTGAGCAAACAAAGAGCA
 AGAAACAAAAAGAAGCCAAGCAGAAGGCTCCAATATGAACAAGATAATCTTCAA
 GACATATTAGAAGTTGGAAAATAATTGATGTGAACTAGACAAGTGTGTTAAGAGTGATAAG
 TAAAATGCACGTGGAGACAAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCCGTACCT
 GGGGAGTGAGAGGACAGGATAGTGCATGTTCTTGTCTGAATTAGTTATATGTGCTG
 TAATGTTGCTCTGAGGAAGCCCCCTGGAAAGTCTATCCAAACATATCCACATCTTATATTCCA
 CAAATTAAAGCTGTAGTATGTACCCCTAACAGACGCTGCTAATTGACTGCCACTCGCAACTCAGG
 GGCGGCTGCATTTAGTAATGGGTCAAATGATTCACTTTATGATGCTTCCAAAGGTGCCT
 TGGCTCTCTTCCAACTGACAAATGCCAAAGTTGAGAAAATGATCATAATTAGCATAAA
 ACAGAGCAGTCGGGGACACCGATTATAAATAACTGAGCACCTTCTTTAAACAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 208

MASLGQILFWSIISIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDI
KLSDIVIQWLKEGVLGLVHEFKEGKDELSSEQDEMFRGRTAVFADQVIVGNASLRLKNVQLTD
AGTYKCYIITSKGKGNANLEYKTGAFSMPEVNVDYNASSETLRCEAPRWFPQPTVVWASQVD
QGANFSEVSNTSFELNSENVTMKVSVLYNVTINNTYSCMIENDIAKATGDIKVTESEIKRR
SHLQLLNSKASLCVSSFFAISWALLPLSPYLMK

FIGURE 209

GAATTTGAGAAGACAGCGCGTGTGCCATGCGGGCGTCTCTGGGCAGGTGTTGGCTCTGGT
 GCTGGTGGCCGCTCTGTGGGTGGCACGCAGCGCTGCTGAAGCGGGCCTCCGCCGGCCTGC
 AGCGGGTTCATGAGCCGACCTGGGCCAGCAGTTGCTACAGGAGATGAAGACCCCTCTTCTG
 AATACTGAGTACCTGATGCCCTTCTCCTCAACCAGTGTGGATCCCTCTATTACCTCAC
 CTTGGCATCGACAGATCTGACCCCTGGCTGTGCCATCTGTAACTCTCTGGCTATCATCTCA
 CACTGATTGTTGGGAAGGCCCTGGAGAAGATATTGGTGGAAAACGTAAGTTAGACTACTGC
 GAGTGCAGGGACGCAGCTCTGTGGATCTGACATACCTGTGTTAGTCCTCCCAGAACCCAT
 CTCCCCAGAGTGGGTGAGGACACGCCCTTCCATCCTGCCCTTCCTCTGCAGCTGTTT
 GCTTCCTGTGCCATCAGAGTCCCTCCCTGGACAGTCTGGAGAAAGACAGAGGCTGG
 GTTGGATGAAGACCAGACCCATCTGAGCCCTCCTCCAGCCCTGTACCAAGCTCCTACT
 GGCATGGCTGAGCTCAGACCCCTCTGATTCTGCCTATTATCCCAGGAGCAGTGCTGGCAT
 GGTGCTCACCGTGATAGGAATTCACTCTGCATCACAGCTCAGTGAGTAAGACCCAGGGC
 AACAGTCTACCCCTTGAGTGGCGAACCCACTTCCAGCTCTGCTGCCTCCAGGAAGCCCT
 GGGCCATGAAGTGCTGGCAGTGAGCGGATGGACCTAGCACTCCCTCTGGCCTAGCTT
 CCTCCTCTTATGGGATAACAGTACCTCATGGATCACAATAAGAGAACAGAGTGAAAG
 AGTTTGTAACCTCAAGTGCTGTCAGCTGCCGGATTAGCACAGGAGACTCTACGCTCA
 CCCTCAGCAACCTTCTGCCAGCAGCTCTTCTGCTAACATCTCAGGCTCCAGCCA
 GCCACCATTACTGTGGCCTGATCTGGACTATCATGGTGGCAGGTTCCATGGACTGCAGAACT
 CCAGCTGCATGAAAGGCCAGCTGCAGACTTGAGCCAGAAATGCAAACGGAGGCCTCTG
 GGACTCAGTCAGAGCGCTTGGCTGAATGAGGGTGGAACCGAGGGAAAGGTGCGTCGGA
 GTGGCAGATGCAGGAAATGAGCTGTCTATTAGCCTGCCTGCCACCCATGAGGTAGGCAG
 AAATCCTCACTGCCAGCCCTCTAAACAGGTAGAGAGCTGTGAGCCCCAGCCCCACCTGAC
 TCCAGCACACCTGGCGAGTAGCTGTCAATAATCTATGAAACAGACAAAAAAA
 AAA

FIGURE 210

MAASLGQVLALVLVAALWGGTQPLLKRASAGLQRVHEPTWAQQLLQEMKTLFLNTEYLMMPFL
LNQCGSLLYYLTLASTDLTLAVPICNSLAIIFTLIVGKALGEDIGGKRKLDYCECGTQLCGS
RHTCVSSFPEPISPEWVRTRPFPLQFCFLVAIRVPFPWTWWRKTEAGVWD

FIGURE 211

CTTCTGTAGGACAGTCACCAGGCCAGATCCAGAAGCCTCTAGGCTCCAGCTTCTGTG
 GAAGATGACAGCAATTATAGCAGGACCCGCCAGGCTGTCGAAAAGATTCCGAATAAAACT
 TTGCCAGTGGGAAGTACCTAGTGAAACGGCCTAACAGATGCCACTTCTCATGTCCCAGGCT
 TGAGGCCCTGTGGTCCCCATCCTTGGGAGAAGTCAGCTCCAGCACC**TGA**AAGGGCATCCTCG
 TTGCTGGTATCACTGCAGTGCTTGCAGCTGTAGAATCTCTGAGCTGCGTGCAGTGTAAAT
 TCATGGAAAAATCCTGTGTCACAGCATTGCCTCTGAATGCCCTCACATGCCAACACCAG
 CTGTATCAGCTCCTCAGCCAGCTCCTCTAGAGACACCAGTCAGATTATACCAAGAATATGT
 TCTGCTAGCGGAGAACTGCAGTGAGGAGACACACATTACAGCCTCACTGTCCACGTGTCT
 GCTGAAGAACACTTCATTTGTAAGCCAGTGCTGCCAAGGAAAGGAATGCAGAACACCAG
 CGATGCCCTGGACCCTCCCTGAAGAACGTGTCCAGCAACGCAGAGTGCCCTGCTTGTATG
 AATCTAATGGAACTTCCTGTCGTGGAGCCCTGAAATGCTATGAAGAACAGTGTGTC
 TTTCTAGTTGCAAGAACTTAAGAACATTGAGTCTAAGAGTCTCGTGTGAAAGGCTGTT
 CAACGTCAGTAACGCCACCTGTCAGTCCCTGTCTGGTGAACAGACTCTGGAGGAGTCA
 TCTTCGAAAGTTGAGTGTGCAAATGTAACAGCTAACCCCCACGTCTGCACCAACCAACT
 TCCCCACAACGTGGCTCCAAAGCTTCCCTTACCTCTGGCCCTGCCAGCCTCTTCTCG
 GGGACTGCTGCC**TGA**GGTCCTGGGCTGCACTTGCCAGCACCCATTCTGCTCTG
 AGGTCCAGAGCACCCCCCTGCGGTGCTGACACCCCTTTCCCTGCTTGCCCCGTTAACTGC
 CCAGTAAGTGGAGTCACAGGTCTCCAGGCAATGCCGACAGCTGCCCTGTTCTCATTATTA
 AAGCACTGGTTCATTCACTGCCAAAAAAAAAAAAAAAAAAAAAA

FIGURE 212

MKGILVAGITAVLVAAVESLSCVQCN SWEKSCVN SIASECP SHANTSCISSSASSSLET PVR
LYQNMFC SAENCSEETHITAFTVHVSAEEHFHFVSQCCQGKECSNTSDALDPPLKNVSSNAE
CPACYESNGTSCRGKPWKCYEEEQCVFLVAELKNDIESKSLVLKGCSNVSNATCQFLSGENK
TLGGVIFRKFECANVNSLTPTSAPTTSHNVGSKASLYLLALASLLL RGLLP

FIGURE 213

GGCCTCGTTCAAACGACCCGGTGGGTCTACAGCGGAAGGGAGGGAGCGAAGGTAGGAGGCA
 GGGCTTGCCTCACTGGCCACCCTCCAACCCAAGAGGCCAGCCCC**ATGGT**CCCCGCCGCCG
 GCGCGCTGCTGTGGGTCTGCTGAATCTGGTCCCCGGCGGGGGCCAAGGCCTG
 ACCCAGACTCCGACCGAAATGCAGCGGTCAAGTTACGCTTGGGGGCCCATGACCCGCAG
 CTACCGGAGCACCGCCGGACTGGTCTTCCCAGAACAGGATAATCCTAGAGGACGAGA
 ATGATGCCATGGCCGACGCCGACCGCCTGGCTGGACCAGCGGCTGCCAGCTTGGCCGCC
 ACGGTGTCCACCGGCTTAGCCGGTCGTCCGCCATTAAACGAGGAGGATGGGTCTTCAGAAGA
 GGGGGTTGTGATTAATGCCGGAAAGGATAGCACCAGCAGAGAGCTTCCCAGTGCAGCTCCCA
 ATACAGCGGGAGTTCCAGCACGAGGTTATAGCCAATAGTCAGGAGCCTGAAATCAGGCTG
 ACTTCAAGCCTGCCCGCTCCCCGGAGGTCTACTGAGGACCTGCCAGGCTCGCAGGCCAC
 CCTGAGCCAGTGGTCCACACCTGGTCTACCCGAGCCGGTGGCCGTACCCCTACCCACAG
 CCATGCCATCTCCTGAGGATCTGCCGCTGGTGCTGATGCCCTGGGCCCCGTGGCACTGCCAC
 TGCAAGTCGGCACCATGAGCCGGAGCCGGTCTGGGAAGCTGCACGCCCTTCCGGCGCCT
 TCGAGTTGGGCGCTGAGCCAGCTCCGCACGGAGCACAGCCTGCACCTATCAACAATGTC
 CCTGCAACCGACTTCGGGAAGAGTGCCCTGGACACAAGTCTGTACTGACACCAACTGT
 GCCTCTCAGAGCACCACCACTACCCCTCCCCACCATCCACCTCAG
 AAGCAGTCCCAGCCTGCCACCCGCCAGCCCTGCCAGCCCTGGCTTTGGAAACGGGTCA
 GGATTGGCCTGGAGGATATTGGAATAGCCTCTTCAGTGTTCACAGAGATGCAACCAATA
 GACAGAAAACCAGAGG**TAA**TGGCCACTTCATCCACATGAGGAGATGTCAGTATCTAACCTCT
 CTTGCCCTTCAATCCTAGCACCCACTAGATTTTAGTACAGAAAAACAAAATGGAAAA
 CACAA

FIGURE 214

MVPAAGALLWVLLNLGPRAGAQGLTQTPTEMQRVSLRFGGPMTRSÝRSTARTGLPRKTRI
ILEDENDAMADADRLAGPAAAELLAATVSTGFSRSSAINEEDGSSEEGVVINAGKDSTSREL
PSATPNTAGSSSTRFIANSQEPEIRLTSSLPRSPGRSTEDLPGSQATLSQWSTPGSTPSRWP
SPSPTAMPSPEDLRLVLMPWGPWHCHCKSGTMSRSRGKLHGLSGRLRVGALSQLRTEHKPC
TYQQCPCNRLREECPLDTSLCDTNCASQSTTSTRTTTPFTIHLRSSPSLPPASPCPALA
FWKRVRIGLEDIWNSLSSVTEMQPIDRNQR

FIGURE 215

CCCGGGT CGACCCACCGTCCGGGAGAAAGG **ATGCCGGCTGGCGCGGTGGTCTGCTAGCTGGGCA**
 GCGGCCTGGCGAGCGGCTCCAGGGCAGCGTGACCGACTGCGTACTGCAGTGCAGAGAGCA
 GAACTGCTCTGGGGCGCTCTGAATCACTCCGCTCCGCCAGCCAATCTACATGAGTCTAGCAGGCTGGACCT
 GTCGGGACGACTGTAAGTATGAGTGATGTGGGTACCGTTGGGCTCACCTCCAGGAAGGTACAAAGTGCCT
 CAGTTCCATGGCAAGTGGCCCTCTCCCGTTCTGGTCTTCAAGAGCGGCATCGGCCGTGCCCTCGTTCT
 CAATGGCCTGGCCAGCCTGGTGTGCTCTGCCGCTACCGCACCTCGTGCAGCCTCCTCCCCCATGTACCA
 CCTGTGTGGCCTTCGCTGGGTGTCCTCAATGCATGGTCTGGTCCACAGTCTTCCACACCAGGGACACTGAC
 CTCACAGAGAAAATGGACTACTTCTGTGCCTCACTGTCATCCTACACTCAATCACCTGTGCTGCGTCAGGAC
 CGTGGGCTGCAGCACCCAGCTGGTCACTGCCTCCGGCTCTCCTGCTGTCATGCTGACCGTGACGTCT
 CCTACCTGAGCCTCATCCGCTCGACTATGGCTACAACCTGGGCCAACGTGGCTATTGGCCTGGTCAACGTG
 GTGTGGTGGCTGGCCTGGTGCCTGTGGAACCAAGCGGGCTGCCACGTGCGCAAGTGCCTGGTGGTGGTCTT
 GCTGCTGCAGGGCTGTCCCTGCTGAGCTGCTGACTTCCCACCGCTCTGGTCCCTGGATGCCATGCCA
 TCTGGCACATCAGCACCATCCGTCCACGTCCTCTTTCACTGGCTTCTGGAAAGATGACAGCCTGTACCTGCTG
 AAGGAATCAGAGGACAAGTCAAGCTGGACT**TGA**AGACCTGGAGCGAGTCTGCCCACTGGGATCCTGCC
 GCCCTGCTGGCCTCCCTCTCCCCCTCAACCCCTTGAGATGATTCTCTTCAACTCTTGAACCTGGACATGA
 AGGATGTGGCCCAGAATCATGTGGCCAGGCCACCCCTGTTGCCCTCACCAGCCTGGAGTCTGTTCTAGGG
 AAGGCCCTCCAGCATCTGGGACTCGAGGTGGCAGCCCTCACCTCTGGAGCTGAACCTGGGTGGAACATGA
 GTGTGTCTTAGCTCTACCGGGAGGACAGCTGCCCTGTTCTCCCCCACCAGCCTCTCCCCACATCCCCAGCTG
 CCTGGCTGGGTCTGAAAGCCCTGTCTACCTGGGAGACCAGGGACACAGGCTTAGGGATACAGGGGTTCCC
 CTTCTGTTACCAACCCCCCACCCCTCCTCAGGACACACTAGTGGTGTGGATGCTGTTCTGGCAGCAA
 GGTTCACGGCGATTCTCCCATGGATCTTGAGGGACCAAGCTGCTGGGATTGGGAAGGAGTTCACCTGACC
 GTTGCCTAGCCAGGTTCCAGGAGGCCACCATACTCCCTTCAGGGCAGGGCTCCAGCAAGCCCAGGGCA
 AGGATCTGTGCTGCTGTCTGGTGAAGAGCCTGCCACCGTGTGTCGGAGTGTGGCCAGGCTGAGTGCATAGG
 TGACAGGGCCGTGAGCATGGCCTGGGTGTGAGCTCAGGCCTAGGTGCGCAGTGTGGAGACGGGTGTGT
 CGGGGAAGAGGTGTGGCTCAAAGTGTGTGTGCAAGGGGTGGGTGTGTTAGCGTGGGTTAGGGAAACGTGT
 TGCCTGCTGGTGGCATGTGAGATGAGTGACTGCCGGTAATGTGTCACAGTTGAGAGGTTGGAGCAGGAT
 GAGGAATCTGTACCACATCAAATCAACTTGAGCGCCAGCTGCCCCAGACGCCACCTGGCGGACAGC
 CAGGAGCTCTCATGGCCAGGCTGCCGTGTGCACTGTTCCCTGTGTTGCCCTTGGCCGCTCTGCAAAC
 CTCACAGGGTCCCCACACACAGTGCCCTCCAGAACGCAAGCAGCCCTCGGAGGCAGAGGAAGGAAAATGGGATGGC
 TGGGCTCTCCATCCTCTTCTGCCATGCCATGGCTGGCCTCCCTCCAAAACCTCCATTCCCC
 GCTGCCAGCCCCCTTGCCATAGCCTGATTTGGGGAGGAGGAAGGGGCGATTGAGGGAGAAGGGGAGAAAAGCT
 TATGGCTGGGTCTGGTTCTCCCTTCCCAGAGGGTCTTACTGTTCCAGGGTGGCCAGGGCAGGCC
 ACACATGCTGTGCCCTGGTAAAGGTGACCCCTGCCATTACAGCAGCCCTGGCATGTTCTGCCACAGG
 AATAGAATGGAGGGAGCTCCAGAAAATTCCATCCAAAGGCAGTCTCCGTGGTTGAAGCAGACTGGATTG
 CTCTGCCCTGACCCCTGTCCCTTTGAGGGAGGGAGCTATGCTAGGACTCCAACCTCAGGGACTCGGGT
 GCCTGCGCTAGCTCTTTGATACTGAAAACCTTTAAGGTGGGAGGGTGGCAAGGGATGTGCTTAATAATCAA
 TTCCAAGCCTCAAAAAAA

FIGURE 216

MAGLAARLVLLAGAAALASGSQGDREPVYRDCVLQCEEQNCSGGALNHFRSRQPIYMSLAGW
TCRDDCKYECMWVTVGLYLQEGHKVPQFHGKWPFSRFLFFQE PASAVASFLNGLASLVMLCR
YRTFVPASSPMYHTCVAFAWVSLNAFWSTVFHTRDLDKMDYFCASTVILHSIYLCVR
TVGLQHPAVVSAFRALLMLTVHVSYLSLIRFDYGYNLVANVAIGLVNVVWWLAWCLWNQR
RLPHVRKCVVVVLLQGLSLLDFPPLFWVLDHAIWHISTIPVHVLFSSLEDDSLYLL
KESEDKFKLD

Important features:

Signal peptide:

amino acids 1-20

Transmembrane domains:

amino acids 105-123, 138-156, 169-185, 193-209, 221-240, 256-272

N-glycosylation site.

amino acids 40-44

N-myristoylation site.

amino acids 43-49

CUB domain proteins profile.

amino acids 285-302

Amiloride-sensitive sodium channels proteins.

amino acids 162-186

FIGURE 217

GGCGCCTGGAATTGGAGTTGTCTGCCACTCGGCTGCCGGAGGCCGAAGGTCCGTGA
 CTATGGCTCCCCAGAGCCTGCCTCATCTAGGATGGCTCCTCTGGCATGCTGCTTGGCTG
 CTGATGCCGCCTGCTCACCTCTGCCTCAGTCATCAGAACCTGAAGGAGTTGCCCTGAC
 CAACCCAGAGAAGAGCAGCACCAAAGAAACGGAGAGAAAAGAAACCAAAGCCGAGGAGGAGC
 TGGATGCCGAAGTCCTGGAGGTGTTCCACCCGACGCATGAGTGGCAGGCCCTCAGCCAGGG
 CAGGCTGTCCCTGCAGGATCCCACGTACGGCTGAATCTCAGACTGGGAAAGAGAGGCAA
 ACTCCAATATGAGGACAAGTTCCGAAATAATTGAAAGGAAAAGGCTGGATATCAACACCA
 ACACCTACACATCTCAGGATCTCAAGAGTCAGTGCCTGGCAAATTCAAGGAGGGGCAGAGATG
 GAGAGTTCAAAGGAAGACAAGGCAAGGCAGGCTGAGGTAAAGCGGCTCTCCGCCATTGA
 GGAAGTGAAGAAAGACTTTGATGAGCTGAATGTTGTCATTGAGACTGACATGCAGATCATGG
 TACGGCTGATCAACAAGTTCAATAGTCCAGCTCCAGTTGGAAGAGAAAGATTGCTGCGCTC
 TTTGATCTGAATATTATGTCCATCAGATGGACAATGCGCAGGACCTGCTTCCTTGGTGG
 TCTTCAAGTGGTGATCAATGGCTGAACAGCACAGAGCCCCTCGTAAGGAGTATGCTGCGT
 TTGTGCTGGCGCTGCCTTCCAGCAACCCCAAGGTCCAGGTGGAGGCCATCGAAGGGGGA
 GCCCTGCAGAAGCTGCTGGTCATCCTGCCACGGAGCAGCCGCTACTGCAAAGAAGAGT
 CCTGTTGACTGTGCTCCCTGCTGCCACTTCCCTATGCCAGCGCAGTTCTGAAGC
 TCGGGGGCTGCAGGTCTGAGGACCTGGTCAGGAGAAGGGCACGGAGGTGCTGCCGTG
 CGCGTGGTCACACTGCTCTACGACCTGGTCACGGAGAAGATGTTGCCAGGAGGAGGCTGA
 GCTGACCCAGGAGATGTCCTCAGAGAAAGCTGCAGCAGTATGCCAGGTACACCTCTGCCAG
 GCCTGTGGAACAGGGCTGGTGCAGATCACGGCCACCTCCTGGCGCTGCCGAGCATGAT
 GCCCGTGAGAACGGTGCAGACACTGGCGCTCCTGACCACCTGCCGGACCGCTACCG
 TCAGGACCCCCAGCTGGCAGGACACTGGCCAGCCTGCAAGGCTGAGTACCAAGGTGCTGGCCA
 GCCTGGAGCTGCAGGATGGTGAGGACGAGGGCTACTTCCAGGAGCTGCTGGCTCTGTCAAC
 AGCTTGCTGAAGGAGCTGAGATGAGGCCCCACACCAGGACTGGACTGGATGCCGCTAGTGA
 GGCTGAGGGGTGCCAGCGTGGTGGCTCTCAGGCAGGAGGACATCTTGGCAGTGCTGGCT
 TGGCCATTAAATGGAAACCTGAAGGCCAAAAA
 AA

FIGURE 218

MAPQLPSSRMAPLGMLLGMAACFTFCLSHQNLKEFALTNPDKTERKETKAEEEL
DAEVLEVFPHTHEWQALQPGQAVPAGSHVRLNLQTGEREAKLQYEDKFRNNLKGKRLDINTN
TYTSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVIETDMQIMV
RLINKFNSSSSSLEEKIAALFDLEYVHQMDNAQDLLSFGGIQQVINGLNSTEPLVKEYAAF
VLGAAFFSSNPKVQVEAIEGGALQKLLVILATEQPLTAKKVLFALCSILLRHFPYAQRQFLKL
GGLQVLRTLVEKGTEVLAVRVVTLLYDLVTEKMFAEEEAELTQEMSPEKLQQYRQVHLLPG
LWEQGWCEITAHLALPEHDAREKVLQTLGVLLTCRDRYRQDPQLGRTLASLQAEYQVLAS
LELQDGEDEGYFQELLGSVNSLLKELR

Important features:

Signal peptide:

amino acids 1-29

Hypothetical YJL126w/YLR351c/yhcX family protein.

amino acids 364-373

N-glycosylation site.

amino acids 193-197, 236-240

N-myristoylation site.

amino acids 15-21, 19-25, 234-240, 251-257, 402-408, 451-457

Homologous region SLS1 protein.

amino acids 68-340

FIGURE 219

TTGGGCTTCCGTAGAGGAAGTGGCGCGGACCTTCATTGGGTTTCGGTCCCCCCCCTCCCC
 CTTCCCCGGGGTCTGGGGTGACATTGCACCGCGCCCTCGTGGGGTCGCCTGCCACCCCA
 CGCGGACTCCCCAGCTGGCGCAGCCCTCCCATTTGCCTGTCTGGTCAGGCCCCCACCCCC
 TTCCCACCTGACCAGCC**TGA**GGGGCTGCAGTCTGGCTGGGACCCGCTCGCGTTATCATCCTGGT
 CGGGCCTTCGCGCTTTCTGATCACTGTGGCTGGGACCCGCTCGCGTTATCATCCTGGT
 CGCAGGGCATTTCCTGGCTGGCTCCCTGGCCTGTGGCTGGTCTGGTCATCTGG
 TCCATGTGACCGACCGGTCAAGATGCCGGTCCAGTACGGCCTCCTGATTTGGTGTGCT
 GTCTCTGTCCTTACAGGAGGTGTCGGCTTGCGCTACTACAAGCTGCTTAAGAAGGCAGA
 TGAAGGGTAGCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGAGATGGCCT
 ATGTTCTGGTCTCTCGGTATCATCAGTGGTGTCTCTGTTATCAATATTTGGCT
 GATGCACTGGGCCAGGTGTTGGGATCCATGGAGACTCACCTATTACTTCCTGACTTC
 AGCCTTCTGACAGCAGCCATTATCCTGCTCCATACCTTTGGGAGTTGTGTTGGATG
 CCTGTGAGAGGAGACGGTACTGGCTTGGCCTGGTGGTTGGAGTCACCTACTGACATCG
 GGACTGACATTCTGAACCCCTGGTATGAGGCCAGCCTGCTGCCATCTATGCACTG
 TTCCATGGGCTCTGGCCTTCATCACAGCTGGAGGGTCCCTCGAAGTATTCAAGCAGCC
 TCTTGTGTAAGGACT**TGA**CTACCTGGACTGATGCCCTGACAGATCCCACCTGCCTGTC
 CCCATGACTGAGCCCAGCCCCAGCCGGTCCATTGCCACATTCTGTCTCCTCTGTC
 GGTCTACCCACTACCTCCAGGGTTTGCTTGTCTTTGTGACCGTTAGTCCTAAAGCTT
 TACCAAGGAGCAGCCTGGGTTAGCCAGTCAGTGACTGGTGGTTGAATCTGCACTATCCC
 CACCAACTGGGACCCCTGTTGTGTCAGGACTCCCCCTGTGTCAGTGCTCTGCTCTCAC
 CCTGCCAAGACTCACCTCCCTCCCCCTGCAAGGCCAGGGCAGGAGGACAGTCGGGTGAT
 GGTGTTCTGCCCTGCGCATCCACCGAGGACTGAGGAACCTAGGGGGACCCCTGGC
 CTGGGGTGCCTCCTGATGTCCTGCCCTGTATTCTCCATCTCCAGTTCTGGACAGTGCA
 GTTGCCAAGAAAAGGGACCTAGTTAGCCATTGCCCTGGAGATGAAATTAAATGGAGGCTCAA
 GGATAGATGAGCTTGAGTTCTCAGTACTCCCTCAAGACTGGACATCTGGTCTTTCTC
 AGGCCTGAGGGGAAACCATTGGTGTGATAAAATACCTAAACTGCCCTTTTTCTTT
 GAGGTGGGGGGAGGGAGGGAGGTATATTGGAACCTCTCTAACCTCCTGGCTATATTCTC
 TCCTCGAGTTGCTCCTCATGGCTGGCTCATTCGGTCCCTTCTCCTGGTCCCAGACCT
 GGGGAAAGGAAGGAAGTGCACTGGGAACTGGCATTACTGGAACATAATGGTTAACCT
 CCTTAACCACCAAGCATCCCTCTCCCCAAGGTGAAGTGGAGGGTGTGGTGAGCTGGC
 CACTCCAGAGCTGCAGTGCACTGGAGGAGTCAGACTACCATGACATCGTAGGGAAGGAGGG
 GAGATTTTTGTAGTTAATTGGGTGTGGAGGGGGGGAGGTTCTATAAAACTG
 ATCATTCTGCTGAGGGTGGAGTGTCCTTAATCAAGGTGATTGTGATTGACT
 AAAAAAAAAGAATTGAAAAAAAAAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAA

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FIGURE 220

MGAAVFFGCTFVAFGPAFALFLITVAGDPLRVIILVAGAFFWLVSLLLASVVWFILVHVTDR
SDARLQYGLLIFGAAVSVLLQEVFVRFAYYKLLKADEGLASLSEDGRSPISIRQMAYVSGLS
FGIISGVFSVINILADALGPGVVGIGHGDSPYYFLTSAFLTAIIILLHTFWGVVFFDACERRR
YWALGLVVGVSHLLTSGLTFLNPWYEASLLPIYAVTSMGLWAFITAGGSLRSIQRSLLCKD

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FIGURE 221

AAGCTGGTTAAGGAAGCAGAGGAGGGTAGATTGAGTGAGGACGGAAGATCAACCCA
TTTCCATTCCGCCAGATGGCCTATGTTCTGGTCTCTCCCTCGGNATCATCAGTGGTGTNT
TNTCTGTTATCAATATTGGCTGATGCANTTGGCCAGGTGTGGTTGGATCCATGGAGAC
TCACCCTATTANTCCTGANTTCAGCCTTNTGACAGCAGCCATTATCCTGCTC

FIGURE 222

GACCGACCCTCAGATGCCCGGTTCCAGTACGGCTCCTGATTTGGTGCTGCTGTNTCTG
TCCTTCTACAGGAGGTGTTCCGCTTGCCTANTACAAGCTGCTTAAGAAGGCAGATGAGGGG
TTAGCATNGCTGAGTGAGGACGGAAGATCACCCATTCCATCCGCCAGATGGCCTATGTTN
TGGTNNTTCCTCGGTATCATCAGTGGTGTNTCTGTTATCAATATTTGGNTGATGCAN
TTGGGCCAGGTGTGGTGGATCCATGGAGANTCACCTATTAAATT CCTGAATT CAGCCTT
NTGACAGCAGCCATTATCCTGNTCCATACCTTGGGGAGTTGTGTTTGATGCCTGTGA
GAGGAG

FIGURE 223

NGTTGGAGAAGTGGCGCGGACNTCATTGGGTTTCGGTTCCCCCTTCCCTTCCCCG
GGGTCTGGGTGACATTGCACGGGCCCTCGTGGGTCGCCTGCCACCCCACGCGGACTCC
CCAGNTGGNGGCCCTTCCCATTGCCTGCTGGTCAGGCCCCACCCCCCTCCCCACNTG
ACCAGCCATGGGGCTCGGGTGTTCGGCTGCACTTCGTCGCGTCGGCCGGCCTCG
CGCTTTCTTGATCACTGTGGCTGGGACCCGCTCGCGTTATCATCCTGGTCGCAGGGCA
TTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGGTCTGGTCATCTGGTCCATGTGAC
CGACCGGTCAAGATGCCCGGCTCCAGTACGGCCTCCTGATTTGGTGCTGCTGCTCTGCC
TTCTACAGGAGGTGTTCCGCTTGCCTACTACAAGCTGCTTAAGAACGGCAGATGAGGGGTTA
GCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTCTGG
TCTCTCCTCGGTATCATCAGTGGTGTCTCTCTGTTATCAATATTTGGCTGATGCACTTG
GGCCAGGTGTGGTTGGGATCCATGGAGACTCACCC

FIGURE 224

GTAAAAGAAAGTGGCCGGACCTTCATTGGGTTTCGGTCCCCCTTCCCNTCCCCGGGG
TCTGGGGGTGACATTGCACCGCGCCNCCTCGTGGGGTGCCTGCCACCCCACGCGGACTCCC
CAGNTGGCGCGCCCTCCCATTGCCTGTCCTGGTCAGGCCCGACCCCCCTCCCACCTGA
CCAGCCATGGGGCTGCGGTGTTTCGGGCTGCACTTCGTCGCGTTGGGCCGGCCTTC
GCGCTTTCTTGATCAGTGTGGCTGGGACCCGCTCGCGTTATCATCCTGGTCGCAGGGC
ATTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGGTCTGGTCATCTGGTCCATGTGA
CCGACCGGTCAAGATGCCCGCTCCAGTACGGCCTCTGATTGGTCTGGTCATCTGGTCCATGTGA
CTTCTACAGGAGGTGTTCCGCTTGCCACTACAAGCTGCTTAAGAAGGCAGATGAGGGTT
AGCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTCTG
GTCTCTCCTTCGGTATCATCAGTGGTCTCTGTTATCAATATTTGGCTGATGCACCTT
GGGCCAGGTGTGGTTGGGATCCATGGAGAC

FIGURE 225

GCCCCAGGGAGCAGTGGGTGGTTATAACTCAGGCCCGTGCCCAGAGCCAGGAGGAGGCAG
TGGCCAGGAAGGCACAGGCCTGAGAAGTCTGCGGCTGAGCTGGGAGCAAATCCCCCACCCCC
TACCTGGGGACAGGGCAAGTGAGACCTGGTGAGGGTGGCTCAGCAGGCAGGGAAAGGAGAGG
TGTCTGTGCGTCTGCACCCACATCTTCTCTGCCCTCCTGCCCTGTCTGGAGGCTGCT
AGACTCCTATCTTCTGAATTCTATAGTGCCCTGGGTCTCAGCGCAGTGCCGATGGTGGCCCGT
CCTTGTGGTCCTCTACCTGGGAAATAAGGTGCAGCGGCCATGGCTACAGCAAGACCCC
CCTGGATGTGGGTGCTCTGTGCTGTGATCACAGCCTGCTTCTGGGGTCACAGAGCATGTT
CTCGCCAACAATGATGTTCTGTGACCACCCCTCTAACACCGTGCCCTCTGGGAGCAACCA
GGACCTGGGAGCTGGGCCGGGAAGACGCCGGTCGGATGACAGCAGCAGCCGATCATCA
ATGGATCCGACTGCGATATGCACACCCAGCCGTGGCAGGCCCGCTTTGCTAAGGCCAAC
CAGCTCTACTGCGGGCGGTGTTGGTGCATCCACAGTGGCTGCTCACGCCGCCACTGCAG
GAAGAAAGTTTCAGAGTCCGTCTCGGCCACTACTCCCTGTACCAGTTATGAATCTGGC
AGCAGATGTTCCAGGGGTCAAATCCATCCCCACCCCTGGCTACTCCCACCCCTGGCCACTCT
AACGACCTCATGCTCATCAAACGTGAACAGAAGAATTGCTCCACTAAAGATGTCAGACCCAT
CAACGTCTCCTCTCATTGTCCTCTGCTGGACAAAGTGCTTGGTGTCTGGCTGGGACAA
CCAAGAGCCCCAAGTGCACCTCCCTAAGGTCCTCAGTGCTTGAATATCAGCGTGTAAAGT
CAGAAAAGGTGCGAGGATGCTTACCGAGACAGATAGATGACACCATTGCTGCCCGGTGA
CAAAGCAGGTAGAGACTCCTGCCAGGGTGATTCTGGGGGCTGTGGTCTGCAATGGCTCCC
TGCAGGGACTCGTGTCTGGGAGATTACCCCTGTGCCCGGCCAACAGACGGGTGTCTAC
ACGAACCTCTGCAAGTTACCAAGTGGATCCAGGAAACCATCCAGGCCACTCCTGAGTCT
CCCAGGACTCAGCACACCGCATCCCCACCTGCTGCAGGGACAGCCCTGACACTCCTTCAG
ACCCTCATTCTCCCAGAGATGTTGAGAATGTTCATCTCTCCAGGCCCTGACCCCCATGTCT
CCTGGACTCAGGGTCTGCTCCCCACATTGGGCTGACCGTGTCTCTAGTTGAACCCCTGG
GAACAAATTCCAAAAGTCCAGGGCGGGGTTGCGTCTCAATCTCCCTGGGCACCTTCAT
CCTCAAGCTCAGGGCCCATCCCTCTGCAGCTGTGACCCAAATTAGTCCCAGAAATAAA
CTGAGAAGTGGAAAAAA

FIGURE 226

MATARPWMWVLCALITALLGVTEHVLANNNDVSCDHPNSNTVPSGSNQDLGAGAGEDARSDD
SSSRIINGSDCDMHTQPWQAALLRPNQLYCGAVLVHPQWLTAHCRKKVFRVRLGHYSLS
PVYESGQQMFQGVKSIPHGYSHPGHSNDIMLIKLNRRIRPTKDVRPINSSHCPAGTKCL
VSGWGTKSPQVHFVQLQCLNISVLSQKRCEDAYPRQIDDTMFCAGDKAGRDSQGDGGP
VVCNGSLQGLVSWGDPARPNRPGVYTNLCKFTKWIQETIQANS

FIGURE 227

ATGGTCAACGACC GG TGG AAG ACC AT GGG CGG C GCT GCC AACT T GAG GACC GG CC GCG CGA
 CAAGCCGCAGCGGCCGAGCTGCGGCTACGTGCTGTGACCGTGCTGCTGGCCCTGGCTGTGC
 TGCTGGCTGTAGCTGTCACCGGTGCCGTGCTCTCCTGAACCACGCCACGCCGGGCACG
 GCGCCCCCACCTGTCGTCAACTGGGGCTGCCAGCGCCAACAGCGCCCTGGTCACTGTGGA
 AAGGGCGGACAGCTCGCACCTCAGCATCTCATTGACCCGCGCTGCCCGACCTCACCGACA
 GCTTCGCACGCCCTGGAGAGCGCCAGGCCCTCGGTGCTGCAGCGCTGACAGAGCACCGGCC
 CAGCCACGGCTGGTGGGGCAGCAGGAGCAGGAGCTGTCAGACGAGTGCATGGGCTGCCGACCAGCTGCC
 CGGCTGCTGGCCGAGCCTCAGAGCTGCAAGACGGAGTGCATGGGCTGCCGAGGGCATG
 GCACGCTGGCCAGGGCCCTCAGCGCCCTGCAAGAGTGAAGCAGGGCCGCTCATCCAGCTCTC
 TCTGAGAGCCAGGGCACATGGCTCACCTGGTGAACCTCCGTCAGCGACATCCTGGATGCCCT
 GCAGAGGGACCGGGGCTGGGCCGCCCGAACAAAGGCCACCTCAGAGAGCGCCCTGCC
 GGGGACCCGGCCCGGGCTGTGCCACTGGCTCCCGCCCGAGACTGTCTGGACGTCTC
 CTAAGCGGACAGCAGGACGATGGCTACTCTGTCTTCCCACCCACTACCCGGCCGGTT
 CCAGGGTGTACTGTGACATGCGCACGGACGGCGGCGCTGGACGGTGTTCAGCGCCGGGAGG
 ACGGCTCCGTGAACCTCTTCCGGGCTGGGACGCGTACCGAGACGGCTTGGCAGGCTCAC
 GGGGAGCACTGGCTAGGGCTCAAGAGGATCCACGCCCTGACCACACAGGCTGCCTACGAGCT
 GCACGTGGACCTGGAGGA CTT GAGAATGGCACGGCTATGCCGCTACGGGAGCTTCGGCG
 TGGGCTGTTCTCGTGGACCCCTGAGGAAGACGGGTACCCGCTACCGTGGCTGACTATTCC
 GGCACTGCAGGGGACTCCCTCCTGAAGCACAGCGGATGAGGTTACCCACCAAGGACCGTGA
 CAGCGACCATTAGAGAACAAACTGTGCCGCTTCTACCGCGGTGCGCACGCCCTATGCCGACGGC
 GCCACACGTCCAACCTCAATGGGAGTACCTGCGCGGTGCGCACGCCCTATGCCGACGGC
 GTGGAGTGGTCTCTGGACCGGTGGCAGTACTCACTCAAGTTCTGTAGATGAAGATCCG
 GCCGGTCCGGGAGGACCGCT**TAG**ACTGGTGCACCTTGTCTTGGCCCTGCTGGTCCCTGTGCG
 CCCATCCCCGACCCACCTCACTTTCGTGAATGTTCTCCACCCACCTGTGCTGGCGAC
 CCACTCTCAGTAGGGAGGGCCGGGCATCCCTGACACGAAGCTCCCTGGGCCGGTGAAGT
 CACACATGCCCTCTCGCCGTCCCCACCCCTCATTGGCAGCTACTGATCTTGCTC
 TGCTGATGGGGCTGGCAAACCTGACGACCCAACTCCTGCCTGCCCTACTGTGACTCCGG
 TGCTGTTGCCGTCCCTGGCCAGGATGGTGGAGTCTGCCCTAGGCACCCCTGCCCCTGCC
 GCCAAATACCGGCATTATGGGACAGAGAGCAGGGGGCAGACAGCACCCCTGGAGTCTC
 CTAGCAGATCGTGGGAATGTCAAGGTCTCTGTAGGTCTGAGGCCAGTATCCTCAG
 CCCTCCAATGCCAACCCCCACCCCTTCCCTGGGCCAGAGAACCCACCTCTCCCCCAA
 GGGCCTAGCCTGGCTGGGCTGGGTGGGCCATCCTACCGGCCCTGAGGTCAAGGATGGG
 GAGCTGCTGCCTTGGGACCCACGCTCCAAGGCTGAGACCACTCCCTGGAGGCCACCC
 CCTGTGCCCGGCAGGCCCTGGGTCTGCAGTCTTACCTGCTGTGCCACCTGCTCTG
 TCTCAAATGAGGCCAACCCATCCCCACCCAGCTCCGGCCGTCTCTACCTGGGCAGC
 CGGGCTGCCATCCCATTCTCCTGCCCTGGAAGGTGGGTGGGCCCTGACCGTGGGCT
 GGACTGCGCTAATGGGAAGCTCTGGTTTCTGGCTGGGCCCTAGGCAGGGCTGGGATGAG
 GCTTGTACAACCCCCACCAATTCCAGGGACTCCAGGGCTCTGAGGTCTCCATGAGGAGGCCAACCTTGC
 GCCTGGGGGTGATGACCCCTTCCCTGAGGTGGCTGTCTCCATGAGGAGGCCAACCTTGC
 ATTGACCGTGGCACCTGGACCCAGGCCAGGGCCAGGCCGGCGAGTGGTCAAGGGACAGGGA
 CCACCTCACCGGCAAATGGGTGGGGGACTGGGCCACAGACGGCACCACCTGGACA
 CTTTCTGTGATGCTCCCAACACCCAGCAGCTGTCACTCCACTCTGTGTCACACA
 TGCAGAGGTGAGACCCGAGGCTCCAGGACCAGCAGCCACAAGGGCAGGGCTGGAGGCCGG
 TCCTCAGCTGTCTGCTCAGCAGCCCTGGACCCCGCGTGCCTACGTCAAGGCCAGATGCAGGG
 CGGCTTTCCAAGGCCTCTGATGGGGCTCCGAAAGGGCTGGAGTCAAGCTGGGAGCT
 GCCTAGCAGCCTCTCTGGGCCAGGAGGGAGGTGGCTTCCCTCCAAAGGACACCCGATGGCA
 GGTGCCCTAGGGGTGTGGGTTCCGTTCCCTCCACTGAAGTTGTGCTTAAA
 AACAAATAATTGACTTGGCACCACTGGGGTTGGAGAGGCCGTGTGACCTGGCTCTC
 TGTCCCAGTGCCACCAGGTATCCACATGCGCAG

FIGURE 228

MVNDRWKTMGAAQLEDRPRDKPQRPSCGYVLCTVLLALAVILLAVENTGAVLFLNHAHAPGT
APPPVVSTGAASANSALVTVERADSSHLSILIDPRCPDLTDSFARLESAQASVQLQALTEHQQA
QPRLVGDQEQLDTLADQLPRLLARASELQTECMGLRKGHGTLGQGLSALQSEQGRLLIQLL
SESQGHMAHLVNSVSDILDALQRDRGLGRPRNKADI.QRAPARGTRPRGCATGSRPRDCLDVL
LSQQQDDGVYVFPTHYPAFQVYCDMRTDGGGWTVFQRREDGSVNFFRGWDAYRDGFGRLT
GEHWLGLKRIHALTTQAAYELHVDLEDFENG TAYARYGSFGVGLFSVDPEEDGYPLTVADYS
GTAGDSILLKHSGMRFTTKDRSDHSENNCAAFYRGAWWYRNCHTSNLNGQYLRGAHASYADG
VEWSSWTGWQYSLKFSEM KIRPVREDR

FIGURE 229

GCAGTCAGAGACTTCCCTGCCCTCGCTGGAAAGAACATTAGGAATGCCTTTAGTGCCT
 TGCTTCTGAACTAGCTCACAGTAGCCCAGGCCCAGGGCAATCCGACCACATTCACACT
 CACCGCTGTAGGAATCCAGTGCAGGCCAAGTACAGCAGCACGAGGGACATGCTGGATGATG
 ATGGGGACACCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACACTCGGCATCCAGAGCCC
 CGGCACAGAGCACAGGGCTCCCTCTCAACGTGGCACCAGTGGCCTGACCCCTGCTGAC
 TTTGTGCTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGCTTTGTTTCACTACTACC
 AGCTCTCAAATACTGGTCAAGACACCATTCTCAAATGGAAGAAAGATTAGGAAATACGTCC
 CAAGAGTTGCAATCTCTCAAGTCCAGAATATAAGCTTGAGGAAGTCTGCAGCATGTGGC
 TGAAAAACTCTGCGTGTGAGCTGTATAACAAAGCTGGAGCACACAGGTGCAGCCCTGTACAG
 AACAAATGGAATGGCATGGAGACAATTGCTACCAAGTTCTATAAGACAGCAAAAGTTGGGAG
 GACTGTAAATATTCTGCCCTAGTGAAAACCTCTACCATGCTGAAGATAAACAAAGAAGA
 CCTGGAATTGCCCGTCTCAGAGCTACTCTGAGTTTCTACTCTTATTGGACAGGGCTT
 TGCGCCCTGACAGTGGCAAGGCCTGGCTGGATGGAACCCCTTCACTCTGAACCTG
 TTCCATATTATAATAGATGTCACCAGCCAAGAACAGAGACTGTGTGGCCATCCTCAATGG
 GATGATCTCTCAAAGGACTGCAAAGAATTGAAGCGTTGTGTGAGAGAACAGGAG
 TGGTGAAGCCAGAGAGCCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGACTGATTGCC
 CTCTGCAACTACAAATAGCAGAGTGAGCCAGGCCAGGCGGTGCCAAGCAAGGGCTAGTTGAGACAT
 TGGGAAATGGAACATAATCAGGAAAGACTATCTCTGACTAGTACAAAATGGTTCTCGTG
 TTCTGTTAGGATCACCAGCATTCTGAGCTGGGTTATGCACGTATTACAGTCACA
 AGAAGTCTTATTACATGCCACCAACCAACCTCAGAAACCCATAATGTCATCTGCCCTCTG
 GCTTAGAGATAACTTTAGCTCTCTCAATGTCTAAATACACCTCCCTGTTTCA
 GTCTCCCTACACTGGTGGAAATAAGAAACTTTGAAGTAGAGGAAATACATTGAGGTAAC
 ATCCTTTCTGACAGTCAAGTAGTCCATCAGAAATTGGCAGTCACCTCCCAGATTGTACC
 AGCAAATACACAAGGAATTCTTTGTTGTTCAGTCATACTAGTCCCTCCAATCCAT
 CAGTAAAGACCCATCTGCCCTGTCATGCCGTTCCAACAGGGATGTCACCTGATATGAG
 AATCTCAAATCTCAATGCCCTATAAGCATTCCCTGTGTCATTAAGACTCTGATAATTG
 TCTCCCTCCATAGGAATTCTCCAGGAAAGAAATATCCCCATCTCCGTTCATATCAG
 AACTACCGTCCCCGATATTCCCTCAGAGAGATTAAAGACCAGAAAAAGTGAGCCTCTCA
 TCTGCACCTGTAATAGTTCACTGCTATTCTCCATTGACCCATATTACACCTTCAG
 GTACTGAAGATTAAATAATAATGTAATAACTGTGAAAAA

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FIGURE 230

MQAKYSSTRDMLDDDGTMSLHSQASATTRHPEPRTTEHRAPSSTWRPVALTLTLCLVLL
IGLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCRE
LYNKAGAHRCSPCTEQWKWHGDNCYQFYKDSKSWECKYFCLSENSTMLKINKQEDLEFAAS
QSYSEFFYSYWTGLLRPDSGKAWLWMDGTPFTSELFHIIDVTSPRSRDCVAILNGMIFSKD
CKELKRCVCERRAGMVKPESLHVPPETLGEGD

FIGURE 231

AATTTCACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGNTGG
ATGATGATGGGACACCACCATGAGCCTGCATTNTCAAGCTTGCACAAATTGGCATCCAG
AGCCCCGGCGCACAGAGCACAGGGNTCCTTTCAACGTGGCGACCAGTGGCCCTGACCCTG
CTGACTTTGTGCTTGGTGCTGCTGATAAGGCTGGCAGCCCTGGGCTTTGTTTCAGTA
CTACCAGCTCTCCAATACTGGTCAAGACACCATTCTCAAATGGAAGAAAGATTAGGAAATA
CGTCCCAGAGTTGCAATTNTCAAGTCCAGAATATAAAGCTTGCAGGAAGTNTGCAGCAT
GTGGCTGAAAAACTCTGCGTAGCTGTATAACAAAGCTGGAGGAACCTTGAAGGAGGGCAA
AGTNTCCTCATNTACTATACACACACCACTCCCC

FIGURE 232

GCCGAGCGCAAGAACCCCTGCGCAGCCCAGAGCAGCTGGAGGGGAATCGAGGCAGCGGGCTC
 CGGGGATTCGGCTCGGGCCGCTGGCTCTGCTCTGCGGGGAGGGAGCAGGGGCCCGCGGGG
 CCCGAGCCCTCGGATCCGCCCCCTCCCCGGTCCCGCCCCCTCGGAGACTCCTCTGGCTGCT
 CTGGGGGTTCGCCGGGGCGGGACCCGGTCCGGCGCC**ATG**CAGGCATCGCTGCTGCTG
 TCGGTGCTGCAGGGCCCGCAGGGCCGTGGCGTGGCATCTCCCTGGCTCACCTGAGCCT
 GCTCAGCGTCACCTGGGTGGAGGAGCGTGCGGCCAGGCCGCCAACCTGGAGACTCTG
 AGCTGCCGCCGCGCAGCAACACCAACGCCGCGCAGGCCAACCTCGGTGCAAGCCGGAGCG
 GAGCGCAGAGAAGCCGGGGCGCGAAGGCCGCCGGAGAAATTGGGAGGCCGCCGCTTGCC
 CTACCACCCCTGCACAGCCCAGGCCAGGCCAAAAAAGGCCGTAGGACCCGCTACATCAGCA
 CGGAGCTGGGCATCAGGCAGAGGCTGCTGGTGGCGTGCTGACCTCTCAGACCACGCTGCC
 ACGCTGGCGTGGCGTGAACCGCACGCTGGGACCGCTGGAGCGTGTGGTGTTCCTGAC
 GGGCGCACGGGGCCGGGGCCCCACCTGGCATGGCAGTGGTGAACGCTGGCGAGGAGCGAC
 CCATTGGACACCTGCACCTGGCGTGCACCTGCTGGAGCAGCACGGCGACGACTTTGAC
 TGTTCTTCTGGTGCCTGACACCACCTACACCGAGGCGCACGGCTGGCACGCCCTAAGTGG
 CCACCTCAGCCTGGCCTCCGCCGCCACCTGTACCTGGGCCGGCCAGGACTTCATCGCG
 GAGAGCCCACCCCGGCCGCTACTGCCACGGAGGCTTGGGGTGTGCTGTCGGCATGCTG
 CTGCAACAACCTGCACCCACCTGGAAGGCTGCCGCAACGACATCGTCACTGGTGAACCGAG
 CGAGTGGCTGGGTGCTGCATTCTCGATGCCACCGGGGTGGCTGCACTGGTGAACCGAG
 GGGTGCACTATAGCCATCTGGAGCTGAGCCCTGGGGAGCCAGTGCAGGAGGGGACCCCTCAT
 TTCCGAAGTGCCTGACAGCCCACCCCTGCGTGACCTGTGCACATGTACAGCTGCACAA
 AGCTTCGCCCGAGCTGAACGACGTACCGTACCGAGGAGATCCAGGAGTTACAGTGGAGA
 TCCAGAAATACCAGCCATCTGGCGTTGATGGGACCGGGCAGCTGCTGGCCCTGGTATT
 CCAGCACCATCCGCCGGCTCCGCTTGAGGTGCTGCGCTGGACTACTTCACGGAGCA
 GCACGCTTCTCTGCGCGATGCTCACCCGCTGCCACTCGCTGGGCTGACCGGGCTG
 ATGTGGCGATGTTCTGGGACAGCTTAGAGGAGCTGAACCGCCGCTACCAACCGGGCTTG
 CGGCTCCAGAAGCAGCAGCTGGTAATGGCTACCGACGCTTGATCCGGCCGGGTATGGA
 ATACACGCTGGACTTGCAGCTGGAGGCACTGACCCCCCAGGGAGGCCGCCGGCCACTC
 GCCGAGTGCAGCTGCTCCGGCGCTGAGCGCGTGGAGATCTTGCCTGTGCCCTATGTC
 GAGGCCTCACGCTCACTGTGCTGCTGCCTCTAGCTGCGGCTGAGCGTGACCTGGCCCTG
 CTTCTGGAGGCCTTGCACCTGCGACACTGGAGCCTGGTGTGCTGCGGAGCCCTGACCC
 TGCTGCTACTGTATGAGCCGCGCAGGCCAGCGCGTGGCCATGCAAGATGTCTCGCACCT
 GTCAAGGCCACGTGGCAGAGCTGGAGCGCGTGGCCAGAGCTGGCCGCTGCCCAGG
 TGTGAGACAGCCGACCCCTCACCACTGCGCCTCATGGATCTACTCTCAAGAACGCC
 TGGACACACTTTCTGCTGGCCGGCCAGACACGGTGCTACGCCCTGACTTCCTGAACCGC
 TGCCGATGCATGCCATCTCCGGCTGGCAGGCCTTCTTCCATGCATTCCAAGCCTCCA
 CCCAGGTGTGGCCCCACACAAGGGCTGGCCCCCAGAGCTGGCCGCTGACACTGGCCGCT
 TTGATGCCAGGCAGCCAGCGAGGCCCTGCTTCTACAACCTCCGACTACGTGGCAGCCGTGG
 CGCCTGGCGGAGCCTCAGAACAAAGAAGAGGAGCTGGAGAGCCTGGATGTGAGGCT
 GTTCTCCACTCTCCAGTCTGCATGTGCTGCGGGCGTGGAGGCCGGCTGCTGCAGCGCT
 ACCGGGCCAGACGTGCAGCGAGGCTCAGTGAGGACCTGTACCAACCGCTGCCCTCAGAGC
 GTGCTTGAGGGCCTCGGCTCCGAACCCAGCTGGCATGCTACTCTTGAACAGGAGCAGGG
 CAACAGCACC**TGA**CCCCACCCCTGTCCCCGTGGCCATGGCACACCCACCCACTT
 CTCCCCAAAACCAGAGGCCACCTGCCAGCCTCGCTGGCAGGGCTGGCGTAGCCAGACCCC
 AAGCTGGCCCACCTGGTCCCCTCTGGCTCTGTGGCTCCCTGGCTCTGGACAAGCACTGGG
 GGACGTGCCAGGCCAGGCCACCCACTTCTCATCCAAACCCAGTTCCCTGCCCTGACGCT
 GCTGATTGGGCTGTGGCTCCACGTATTATGCAAGTACAGTCTGCCTGACGCCAGCCCTGC
 CTCTGGGCCCTGGGGCTGGCTGTAGAAGAGTTGGGGAGCTGAGGAGGG
 GCATCTCCAACTTCTCCCTTTGGACCCCTGCCAGCTCCCTGCCTTAATAAAACTGGCCA
 AGTGTGGAAAAA

DRAFT - NOT FOR CITATION

FIGURE 233

MRASLLSVLRPAGPVAVGISLGFTLSLLSVTWEEPAGPGPQPGDSELPPRGNTNAARRP
NSVQPGAEREKPGAGEGAGENWEPRVLPYHPAQPGQAACKAVRTRYISTELGIRQRLLVAVL
TSQTLPTLGAVNRTLGHRLERVVFLTGARGRRAPPMAVVTLGEERPIGHLHLALRHILLE
QHGDDFDWFVLPDTTYTEAHGLARLTGHLASAAHLYLGRPQDFIGGEPTPGRYCHGGFG
VLLSRMILQQLRPHLEGCRNDIVSARPDEWLGRCILDATGVGCTGDHEGVHYSLELSPGEP
VQEGDPHFRSALTAHPVRDPVHMYQLHKAFARAELEYQEIQELOWEIQNTSHLAVGDRA
AAWPVGIPAPSRRPASRFEVLRWDYFTEQHAFSCADGSPRCPLRGADRADVADVLGTALEELN
RRYHPALRLQKQQLVNGYRRFDPARGMEYTLDLQLEALTPQGGRRPLTRVQLRPLSRVEI
LPVPYVTEASRLTVLLPLAAAERDLAPGFLEAFATAALEPGDAAAALTLLLLYEPRQAQRVA
HADVFAVKAHVAELERRFPGARVPWLSVQTAAPSPLRLMDLLSKKKPLDTLFLLAGPDTVL
TPDFLNRCRMHAISGWQAFFPMHFQAFHPGVAPPQGPGPPELGRDTGRFDRQAASEACFYNS
DYVAARGRLAAASEQEEELLESLDVYELFLHFSSLHVLRAVEPALLQRYRAQTC SARLSEDL
YHRCLQSVLEGLGSRTQLAMLLFEQEQQNST

FIGURE 234

GCTCTGGCGGCCCGGCGATTGGTCACCGCCCGTAGGGGACAGCCCTGGCCTCCTTGAT
TGGCAAGCGCTGGCACCTCCCCACACCCCTTGCAGACGCTCCCCTAGTGGAGAAAAGGAGT
AGCTATTAGCCAATTGGCAGGGCCCGTTTTAGAAGCTTGATTCCTTGAAAGATGAAAG
ACTAGCGGAAGCTCTGCCTCTTCCCCAGTGGCGAGGGAACTCGGGCGATTGGCTGGAA
CTGTATCCACCCAAATGTCACCGATTCTCCTATGCAGGAAATGAGCAGACCCATCAATAA
GAAATTCTCAGCCTGGCCGAAATGGTGGCCCCACGAAGCCACGACAACGGAGGCAAAG
AGGGTTGCTCAACGCCCCGCTCATTGGAAAACCAAATCAGATCTGGACCTATAGCGTG
GCGGAGGCAGGGCGATGATTGTCGCGCTCGCACCCACTGCAGCTGCGCACAGTCGCTTCT
TTCCCCGCCCCCTGAGACCCTGCAGCACCATCTGTC**ATG**GCAGCTGGCTGTTGGTTGAGC
GCTCGCCGTCTTGGCGGCAGCGCGACGGCAGGGCTCCGGCCCGCGTCCGCTGGGA
ATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCTGTGGCGGGAAAGCGGCCCCAGAAC
CGACACACCGTGGCAAGAGGACCCAGAACCCGAGGACGAAAATGTATGAGAAGAACCA
GAATGGTATGACAAGGACCCGTTGGACGTCTGGAACATGCACTGTCTTCTT
CTTGCGTCTCCATCATCCTGGCCTTGGCAGCACCTTGTGGCTATGCGCTGACTACA
GGATGAAAGAGTGGTCCCGCCGCAAGCTGAGAGGCTGTGAAATACCGAGAGGCCAATGGC
CTTCCCATCATGGAATCCAATGCTTCGACCCAGCAAGATCCAGCTGCCAGAGGATGAG**TG**
ACCAGTTGCTAAGTGGGCTCAAGAAGCACCGCCTCCCCACCCCTGCCTGCCATTCTGAC
CTCTTCTCAGAGCACCTAATTAAAGGGCTGAAAGTCTGAA

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FIGURE 235

MAAGLFGLSARRLLAAAATRGLPAARVRWESSFSRTVVAPS A VAGKRPEPTTPWQEDPEPE
DENLYEKNPDSHGYDKDPVLDVWNMRLVFFFGVSIILVLGSTFVAYLPDYRMKEWSRREAER
LVKYREANGLPIMESNCFDPSKIQLPEDE

FIGURE 236

GGCGGCTGGCTTTGGTTGAGCGCTGCCGTCTTGGCGCAGCGCGACGCGAGGGC
TCCCGGCCGCCCGTCCGCTGGGAATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCT
GTGGCGGGAAAGCGGCCCGAACCGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGA
CGAAAATTGTATGAGAAGAACCCAGACTCCCATGGTTATGACAAGGACCCGTTTGGACG
TCTGGAACATGCGACTTGTCTTCTTGGCGTCTCCATCATCCTGGTCCTGGCAGCACC
TTTGTGGCCTATCTGCCTGACTACAGGATGAAAGAGTGGTCCGCCCGAAGCTGAGAGGCT
TGTGAAATACCGAGAGGCCAATGGCCTCCATCATGGAATCCAAGTCTCGACCCAGCA
AGATCCAG

FIGURE 237

GCGGCGGCT**ATG**CCGCTTGCTCTGCTCGTCCGTGCTCTGGGGCCGGCGGCTGGTGCCT
 TGCAGAACCCCCACGCGACAGCCTGCGGGAGGAACTTGTCATCACCCCGCTGCCTCCGGGG
 ACGTAGCCGCCACATTCCAGTTCCGCACGCGCTGGGATTCGAGCTTCAGCGGGAAAGGAGTG
 TCCCATTACAGGCTCTTCCCAAAGCCCTGGGGCAGCTGATCTCAAGTATTCTCTACGGGA
 GCTGCACCTGTCATTACACAAGGCTTTGGAGGACCCGATACTGGGGGCCACCTCCTGC
 AGGCCCATCAGGTGCAGAGCTGTTCTGGGTTCCAAGACACTGTCACTGATGTGGATAAA
 TCTTGAAGGAGGCTCAGTAATGTCCTCTCAGGGATCTTCTGCGCCTCTCAACTCATCGA
 CTCCACCAACACAGTCACTCCCAC TG CCT CTT CAA ACCCCTGGGTCTGCCAATGACACTG
 ACCACTACTTCTGCGCTATGCTGTGCTGCCGCGGGAGGTGGTCTGCACCGAAAACCTCACC
 CCCTGGAAGAAGCTCTGCCCCTGAGTTCCAAGGCAGGCCTCTGTGCTGCTGAGGAGA
 TCGCTTGTCCACACCAGCTACCACTCCCAGGCAGTCATATCCGCCCTGTTGAGAAATG
 CACGCTGTACTAGCATCTCCTGGGAGCTGAGGCAGACCCCTGTCAGTTGATTTGATGCCCTC
 ATCACGGGGCAGGGAAAGAAAGACTGGTCCTCTCCGGATGTTCTCCGAACCCCTCACCGA
 GCCCTGCCCTGGCTCAGAGAGCCGAGTCTATGGACATCACCACCTACAACCAGGACA
 ACGAGACATTAGAGGTGCACCCACCCCCGACCACTACATATCAGGACGTCACTCTAGGCAC
 CGGAAGACCTATGCCATCTATGACTTGCTTGACACCGCCATGATCAACAACTCTCGAAACCT
 CAACATCCAGCTCAAGTGGAAAGAGACCCCCAGAGAATGAGGCCCCCAGTGCCTCCTGC
 ATGCCAGCGGTACGTGAGTGGCTATGGGCTGCAAGGGGAGCTGAGCACACTGCTGTAC
 AACACCCACCCATACCAGGGCCTTCCCGGTGCTGCTGGACACCGTACCTGGTATCTGCG
 GCTGTATGTGCAACACCCCTACCACACCTCAAGGGCAAGGAGAACAAACCAAGTTACATCC
 ACTACCAGCCTGCCAGGACCGGCTGCAACCCCCACCTCCTGGAGATGCTGATTCACTGCCG
 GCCAACTCAGTCACCAAGGTTCCATCCAGTTGAGCGGGCGCTGCTGAAGTGGACCGAGTA
 CACGCCAGATCTAACCATGGCTCTATGTCAGCCCATCTGTCCTCAGGCCCTGTGCCCA
 GCATGGTAGCAGCCAAGCCAGTGGACTGGGAAGAGAGTCCTCTTCAACAGCCTGTTCCA
 GTCTCTGATGGCTCTAACTACTTGTGCGGCTCTACACGGAGCCGCTGCTGGTGAACCTGCC
 GACACCGGACTTCAGCATGCCCTACACGTGATCTGCCCTACGTGCACTGTTGGCCGTGT
 GCTACGGCTCCTCTACAAATCTCCTCACCCGAACCTTCCACATCGAGGAGGCCGCACAGGT
 GGCCTGGCCAAGCGGCTGGCCAACCTTATCCGGCGCGCCCGAGGTGTCCCCCACT**TGATT**
 CTTGCCCTTCCAGCAGCTGCAGCTGCCGTTCTCTGGGGAGGGGAGCCAAAGGGCTGTT
 TCTGCCACTTGTCTCCTCAGAGTTGGCTTTGAACCAAAGTGCCTGGACCGAGTCAGGGC
 CTACAGCTGTGTTCCAGTACAGGAGCCAGGCAAATGTGGCATTGAATTGAATTAA
 CTTAGAAATTCTACCTGCTGAGTGGCCACCTCTATATTGAGGTGCTCAATAAGCAAA
 AGTGGTCGGTGGCTGCTGTATTGGACAGCACAGAAAAAGATTCCATCACCACAGAAAGGTC
 GGCTGGCAGCACTGGCAAGGTGATGGGGTGTGCTACACAGTGTATGTCACTGTGAGTGG
 TGGAGTTACTGTTGTGAATAAAAACGGCTGTTCCGTGGAAAAAAAAAAAAA

FIGURE 238

MPLALLVLLLLGPWGCLAEPPRDSLREELVITPLPSGDVAATFQFRTRWDSELQREGVSHY
RLFPKALGQLISKYSLRELHLSFTQGFWRTRYWGPPFLQAPSGAELWVWFQDTVDVDSWK
ELSNVLSGIFCASLNFIIDSTNTVPTASFKPLGLANDTDHYFLRYAVLPREVVCTENLTPWK
KLLPCSSKAGLSVLLKADRLFHTSYHSQAVHIRPVCRNARCTSISWELRQTLSVVFDAFITG
QGKKDWSLFRMFSRTLTEPCPLASESRVYDITTYNQDNETLEVHPPPTTYQDVILGTRKT
YAIYDLLDTAMINNSRNLNIQLKWKRPPENEAPPVPFLHAQRYVSGYGLQKGELSTLLYNTH
PYRAFPVLLLDTPWYLRLYVHTLTITSKGKENKPSYIHYQPAQDRLQPHLLEMLIQLPANS
VTKVSIQFERALLKWTEYTPDPNHGFYVSPSVLSALVPSMVAAKPVDWEESPLFNSLFPVSD
GSNYFVRLYTEPLLVLNLPDFSMPPNVICLTCTVVAVCYGSFYNLLRTFHIEEPRTGGLA
KRLANLIRRARGVPPL

FIGURE 239

CAACATGGGGTCCAGCAGCTTCTGGTCCTCATGGTGTCTCGTTCTGTGACCCTGGTGG
CTGTGGAAGGAGTTAAAGAGGGTATAGAGAAAGCAGGGGTTGCCAGCTGACAACGTACGC
TGCTTCAAGTCCGATCCTCCCCAGTGTACACAGACCAGGACTGTCTGGGGAAAGGAAGTG
TTGTTACCTGCACTGTGGCTTCAAGTGTGATT CCTGTGAAGGA ACTGGAAGAAGGAGGAA
ACAAGGATGAAGATGTGTCAAGGCCATACCC TGAGCCAGGATGGGAGGCCAAGTGTCCAGGC
TCCTCCTCTACCAGGTGCCTCAGAAATGATGCTGGTCCTTCTACCTCTGGGGTCAC
TCAC TTGGCACCTGCCCTGAGGGCTTGAGACTT GGAAT ATGGAAGAAGCAATACCCACC
CCACCAAAGAAAACCTGAGCTTGAAGTCCTTCCC AAAAAGAGGGAAAGAGTCACAAAAG
TCCAGACCCCAGGGACGGTACTTCCCTCTACCTGGTGCCTCCCTAATGCTCATGAAT
GGACCCCTCATGAATGAAACCAGTGCCTTATAAGAGACCCCAAAGAGAGCTGCCTGCCCTC
TGCAATGTGTGATCACAGCTAGAAGGCACTGT CAGAGAAGAGAAACTGGTCCCTCACCAGATG
CTGAATCTGCTGGTGCCTTGATCTGGACTTCCCAGCCTCTAGAACTGTAAGAAATAATAT
TTGCTGTTATAATCCAA

FIGURE 240

MGSSSFLVLMVSLVLVTLVAVEGVKEGIEKAGVCPADNVRCFKSDPPQCHTDQDCLGERKCC
YLHCGFKCVIPVKELEEGGNKDEDVSRPYPEPGWEAKCPGSSSTRCPQK

Signal sequence:

amino acids 1-19

N-myristoylation sites:

amino acids 23-29, 27-33, 32-38, 102-108

WAP-type 'four-disulfide core' domain signature:

amino acids 49-63

FIGURE 241

AAACTCAGCACTGCCGGAGTGGCTCATTGTTAAGACAAAGGGTGTGCACCTCCGCCAGG
 AAACCTGAGCGGTGAGACTCCCAGCTGCCTACATCAAGGCCCAAGGACATGCAGAACCTCC
 TCTAGAACCGACCCACCAC**ATG**AGGTCTGCCTGGAGATGCAGGCACCTGAGCCAAGG
 CGTCCAGTGGTCCTGCTCTGGCTGCTGGTCTTCTTCTTCGCCTGCCCTTTTA
 TTAAGGAGCCTCAAACAAAGCCTTCCAGGCATCAACGCACAGAGAACATTAAAGAAAGGTCT
 CTACAGTCCCTGGCAAAGCTAAGTCCCAGGCACCCACAAGGGCGAGGAGGACAACCATCTA
 TGCAGAGCCAGGCCAGAGAACAAATGCCCTAACACACAAACCAAGGCCAACACCA
 CCGGAGACAGAGAACAGGAGGCCAACAGGCACCGCCGGAGGAGCAGGACAAGGTGCCAC
 ACAGCACAGAGGGCAGCATGGAAGAGCCCAGAAAAAGAGAACCATGGTGAACACACTGTC
 ACCCAGAGGGCAAGATGCAGGGATGGCCTCTGGCAGGACAGAGGCACAATCATGGAAGAGCC
 AGGACACAAAGACGACCCAAGGAATGGGGCCAGACCAGGAAGCTGACGGCCTCCAGGACG
 GTGTCAGAGAACGACCAGGGCAAAGCGGCAACCACAGCAAGACGCTCATTCCAAAAGTCA
 GCACAGAAATGCTGGCTCCCACAGGAGCAGTGTCAACAAGGACGAGACAGAAAGGAGTGACCA
 CAGCAGTCATCCACCTAAGGAGAACCTCAGGCCACCCACCCCTGCCCTTCCAG
 AGCCCCACGACGAGAACAAAGACTGAAGGCCAACCTCAAATCTGAGCCTCGTG
 GGATTTGAGGAAAAATACAGCTCGAAATAGGAGGCCTCAGACGACTGCCCTGACTCTG
 TGAAGATCAAAGCCTCCAAGTCGCTGTGGCTCCAGAAACTCTTCTGCCAACCTCACTCTC
 TTCCTGGACTCCAGACACTCAACCAGAGTGAGTGGGACCGCCTGGAACACTTGCACCACC
 CTTTGGCTTCATGGAGCTCAACTACTCCTGGTGCAGAAGTCGTGACACGCTCCCTCCAG
 TGCCCCAGCAGCAGCTGCTCCTGGCCAGCCTCCCGCTGGGAGCCTCCGGTGCATCACCTGT
 GCCGTGGTGGGCAACGGGGCATCCTGAACAACCTCCCACATGGGCAGGAGATAGACAGTCA
 CGACTACGTGTTCCGATTGAGCGGAGCTCTCATTAAAGGCTACGAACAGGATGTGGGACTC
 GGACATCCTCTACGGCTTACCGCCTCTCCCTGACCCAGTCACTCCTTATATTGGCAAT
 CGGGGTTCAAGAACGTGCCTCTGGGAAGGACGTCCGCTACTGCACTCCTGGAAAGGCAC
 CCGGGACTATGAGTGGCTGGAAGCACTGCTTATGAATCAGACGGTGATGTCAAAAAACCTT
 TCTGGTTCAAGGCCACAGACCCAGGAAGCTTTCGGGAAGGCCCTGCACATGGACAGGTACCTG
 TTGCTGCACCCAGACTTCTCCGATACTGAAGAACAGGTTCTGAGGTCTAAGACCCCTGGA
 TGGTGCCCACTGGAGGATATACCGCCCAACTGGGCCCTCTGCTGCTCACTGCCCTC
 AGCTCTGTGACCAGGTGAGTGCTTATGGCTCATCACTGAGGCCATGAGCGCTTCTGAT
 CACTACTATGATACATCATGGAAGCGGCTGATCTTACATAAACCATGACTCAAGCTGGA
 GAGAGAAGTCTGGAAGCGGCTACAGATGAAGGGATAATCCGGCTGTACCGCGTCTGGTC
 CCGGAACGTGCCAAAGCCAAGAAC**TGA**CCGGGGCCAGGGCTGCCATGGCTCCTGCCCTGCTC
 CAAGGCACAGGATAACAGTGGAAATCTTGAGACTCTTGGCCATTCCATGGCTCAGACTAA
 GCTCCAAGCCCTCAGGAGTTCCAAGGGAACACTTGAACCATGGACAAGACTCTCAAGAT
 GGCAAAATGGCTAATTGAGGTTCTGAAGTTCTCAGTACATTGCTGTAGGTCTGAGGCCAGG
 GATTTTAATTAAATGGGTGATGGTGGCCAATACCACAATTCTGCTGAAAAACACTCTT
 CCAGTCCAAAAGCTTCTGATACAGAAAAAGAGCCTGGATTACAGAAACATATAGATCTG
 GTTGAAATTCCAGATCGAGTTACAGTTGAAATCTGAAGGTATTACTTAACCTCACTAC
 AGATTGTCTAGAAGACCTTCTAGGAGTTCTGATTCTAGAAGGGTCTATACTTGTCCCTG
 TCTTTAAGCTATTGACAACCTACGTGTTGTAGAAAACGTGATAATAACAAATGATTGTT
 GTCCATGGAAAGGCAAATAAATTCTACAGTGAACAAAAAA

FIGURE 242

MRSCLWRCCRHLSQGVQWSLLLAVLVFFLFALPSFIKEPQTKPSRHQRTENIKERSLQSLAKP
KSQAPTRARRTTIYAEPAPEENNALTQPKAHTTGDRGKEANQAPPEEQDKVPHTAQRAAW
KSPEKEKTMVNTLSRGQDAGMASGRTEAQSWKSQDTKTTQGNGGQTRKL TASRTVSEKHQG
KAATTAKTLIPKSQHRLMLAPTGA VSTRTRQKGVT TAVIPPKEKKPQATPPPAPFQSPTTQRN
QLKAANFKSEPRWD FEEKYSFEIGGLQTTCPDSVKIKASKSLWLQKLFLPNLTFLDSRHF
NQSEWDRLEHFAPPFGFMELNYSLVQKV VTRFPPV PQQQLLLASLPAGSLRCITCAVVGNGG
ILNNSHMGQEIDSHDYVFR LSGALIKGYEQDV GTRTSFYGFTAFSLTQSLLILGNRGFKNVP
LGKDVRYLHFLEGTRDYEWLEALLMNQTVMSKNLFWFRHRPQEAFREALHMDRYLLLHPDFL
RYMKNRFLRSKTLDGAH WRIYRPTTGALLLTALQLCDQVSAYGFITEGH ERFSDHYY DTSW
KRLIFYINHDFKLEREVWKRLHDEGIIRLYQRPGPGTAKAKN

Cytoplasmic Domain:

amino acids 1-10

Type II Transmembrane Domain:

amino acids 11-35

Lumenal catalytic Domain:

amino acids 36-600

Ribonucleotide Reductase small subunit Signature:

amino acids 481-496

N-glycosylation Sites:

amino acids 300-303, 311-314, 331-334, 375-378, 460-463

FIGURE 243

CGATGCGCGGACCCGGGACCCCTCCTGGGCTGCTGCTGGTGC~~T~~GGCCTCGCCG
GAGCAGCGAGTGGAAATTGTTCCCTCGAGATCTGAGGATGAAGGACAAGTTCTAAAACACCT
TACAGGCCCTTTATTTAGTC~~AA~~GTGCAGCAAACACTCCATAGACTTATCACAACA
CCAGAGACTGCACCATTCTGCATACTATAAAAGATGCGCCAGGCTTACCCGGCTGGCT
GTCAGTCCAGTGTGCATGGAGGATAAGTGAGCAGACCGTACAGGAGCAGCACACCAGGAGCC
ATGAGAAGTGCCTGGAAACCAACAGGGAAACAGAACTATCTTATACACATCCCCTCATGG
ACAAGAGATTATTTGCAGACAGACTCTCCATAAGTCCTTGAGTTGTATGTTGTTG
ACAGTTGCAGATATATTCGATAAATCAGTGTACTGACAGTGTATCTGTCACTTATT

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FIGURE 244

MRGPGHPLLGLLLVLGPSPEQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKFHRLYHNT
RDCTIPAYYKRCARLLTRLAVSPVCMEDK

FIGURE 245

GGGCTGGCCCCGCCAGCTCCAGCTGGCCGGCTTGGTCCTGCGGTCCCTCTGGGAGG
CCCGACCCGGCGCCCAGCCCCAACCAATGCCACCCGCGGGCTCCGCCGGCGGCCG
CTCACCGAATCGCTCTGTTGGTGCCTGGCATCCGGGTTAACTGCGAGTTCTCACCTCT
GTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGTTAACTGCGAGTTCTCACCTCT
GCTGCAGGACCTGCTACCACATCGGTACTGCTGCAGGGACCTGACCTGCTTATCACCGAGAGG
CAGCAGAACGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATGCCTCAGCTGTGAT
CCTCTTGTTGCTGTGGTGCACCACCATCTGCTGCTTCCTCTGTTCTGCTACCTGT
ACCGCCGGCGCCAGCAGCTCCAGAGCCCATTGAAGGCCAGGAGATTCCAATGACAGGCATC
CCAGTGCAGCCAGTATAACCCATACCCCCAGGACCCAAAGCTGGCCCTGCACCCCCACAGCC
TGGCTTCATGTACCCACCTAGTGGCCTGCTCCCCAATATCCACTCTACCCAGCTGGCCCC
CAGTCTACAACCCCTGCAGCTCCTCCCTATATGCCACCACAGCCCTTACCCGGGAGCC
TGAGGAACCAAGCCATGTCTCTGCTGCCCTTCAGTGATGCCAACCTGGGAGATGCCCTCAT
CCTGTACCTGCATCTGGCCTGGGGTGGCAGGAGTCCTCCAGCCACCAGGCCAGACCAA
GCCAACCCCTGGGCCCTACTGGGACAGAGCCCCAGGGAAGTGGAACAGGAGCTGAACTAGA
ACTATGAGGGTTGGGGGAGGGCTTGAATTATGGCTATTTACTGGGGCAAGGGAGG
GAGATGACAGCCTGGTCACAGTGCCTGTTCAAATAGTCCCTGCTCCAAAGATCCAG
CCAGGAAGGCTGGGCCCTACTGTTGTCCTCTGGCTGGGTGGGGAGGGAGGGAGGAGGT
TCCGTCAGCAGCTGGCAGTAGCCCTCCTCTGGCTGCCCACTGGCCACATCTCTGGCCTG
CTAGATTAAAGCTGTAAAGACAAAA

FIGURE 246

MPPAGLRRAAPLTAAIALLVLGAPLVLAGEDCLWYLDRNGSWHPGFNCEFFTFCGGTCYHRYC
CRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCFLCSCCYLYRRRQQLQSP
FEGQEIPMTGIPVQPVYPYPQDPKAGPAPPQPGFMYPPSGPAPQYPLYPAGPPVYNPAAPPP
YMPPQPSYPGA

Transmembrane Domains:

amino acids 10-28, 85-110

N-glycosylation Site:

amino acids 38-41

N-myristoylation Sites:

amino acids 5-10, 88-93

FIGURE 247

GGGGGAGCTAGGCCGGCGCAGTGGTGGTGGCGGCAGCAAGGGTGAGGGCGGCCAGAA
 CCCCAGGTAGGTAGAGCAAGAAG**ATG**GTTTCTGCCCTCAAATGGTCCCTGCAACCAG
 TCATTTCTACTTCCTCACTGTTGGCTCTCTTAACGTGTCCACTCCTCATGGTGTAGAG
 CACTGAAGCATCTCCAAAACGTAGTGATGGACACCATTTCTGGAAATAAACACGACTTC
 CTGAGTAGTCATCCCAGTCATTATGATCTCTGATCCATGCAAAACCTTACCAACGCTGACC
 TTCTGGGAACACAGAAGTAGAAATCACAGGCCAGTCAGGCCACCCAGCACCACATCCTGCA
 TAGTCACCACCTGCAGATATCTAGGGCCACCTCAGGAAGGGAGCTGGAGAGAGGCTATCGG
 AAGAACCCCTGCAGGTCTGGAACACCCCCCTCAGGAGCAAATGCACTGCTGGCTCCCGAG
 CCCCTCTTGTGGGCTCCGTACACAGTTGTCATTCACTATGCTGGCAATCTTCGGAGAC
 TTTCCACGGATTTCACAAAGCACCTACAGAACCAAGGAAGGGAACTGAGGATACTAGCAT
 CAACACAATTGAAACCCACTGCAGCTAGAAATGGCCTTCCCTGCTTGATGAACCTGCCTC
 AAAGCAAGTTCTCAATCAAATTAGAAGAGAGCCAAGGCACCTAGCCATCTCAAATATGCC
 ATTGGTGAATCTGTGACTGTTGCTGAAGGACTCATAGAACGACATTGATGTCACTGTGA
 AGATGAGCACCTATCTGGTGGCCTCATCATTTCAGATTGAGTCTGTCAGCAAGATAACC
 AAGAGTGGAGTCAGGTTCTGTTATGCTGTGCCAGACAAGATAATCAAGCAGATTATGC
 ACTGGATGCTGCCGTGACTCTCTAGAATTATGAGGATTATTCAGCATACCGTATGGAAA
 TACCCAAACAAGATCTTGTGCTATTCCGACTTCAGTCAGTCTGGCTATGGAAA
 CTGACAAACATATAGAGAACCTGCTCTGTTGATGCAGAAAAGCTTCTGCATCAAGTAA
 GCTTGGCATCACAGTGAATGTTGCTGTTGATGCAGAAAAGCTTCTGCATCAAGTAA
 CTATGGAATGGTGGAAATGATCTTGGCTAAATGAAGGATTGCCA
 TCTGTCAGTGTGACCCATCTGAACGAAAGTTGGAGATTATTCCTGGCAAATGTTGA
 CGCAATGGAGTAGATGCTTAAATTCTCACACCCCTGTGTCACACCTGTGGAAA
 CTCAGATCCGGGAGATGTTGATGATGTTCTTATGATAAGGGAGCTGTATTCTGAATATG
 CTAAGGGAGTATCTAGCGCTGACGCATTAAAAGTGGTATTGTCAGTATCTCAGAAC
 TAGCTATAAAACAAAAACGAGGACCTGTGGGATAGTATGGCAAGTATTGCCCTACAG
 ATGGTAAAAGGGATGGATGGCTTGTCTAGAACATTCACTCTCACAT
 TGGCATTGAGAACACTGGACACTGCAGAGGGTT
 TCCCCTAATAACCACAGTGAGGGGGAGGAATGTACACATGAAGAACAGCAGTACATGA
 AGGGCTCTGACGGCGCCCGGACACTGGGTACCTGTGGCATGTCATTGACATTCA
 AGCAAATCCAACATGGTCCATCGATTGCTAAAACAAAAACAGATGTGCTCATCCTCCC
 AGAACAGGGTGGATGGATCAAATTAAATGTGGGATGAATGGCTATTACATTG
 AGAAGAGGATGGGCTTGTGAAACACACACAGCAGTCAGCAGT
 AGGATGGGATGGGACTCTTGACTGGCTTTAAAAGGAACACACAGCAGTCAGCAGT
 AATGATCGGGCAAGTCTTAACAATGCATTTCAGCTCGTCAGCATGGGAAGCTGTCCAT
 TGAAAAGGCCTGGATTTCCTGTACTTGAAACATGAAACTGAAATTATGCCGTGTT
 AAGGTTGAATGAGCTGATTCTATGTATAAGTTAATGGAGAAAAGAGATATGAATGAAGTG
 GAAACTCAATTCAAGGCCTTCCTCATCAGGCTGCTAAGGGACCTCATGATAAGCAGACATG
 GACAGACGAGGGCTCAGTCTCAGAGCAAATGCTGCCAGTGAACACTACTCCTGCCGTG
 TGCACAACATCAGCCGTGCGTACAGAGGGCAGAAGGCTATTCAGAAAAGTGGAGGAAG
 AATGGAAA
 ACTTGAGCCTGCCTGCGACGCTTGGCAGTTGCTGTGGGGGCCAGAG
 CACAGAAGGCTGGGATTCTTATAGTAAATATCAGTTCTTGTGCTCAGTACTGAGAAA
 GCCAAATTGAATTGCCCTCTGCAGAACCCAAAATAAGGAAAAGCTTCATGGCTACTAGAT
 GAAAGCTTAAGGGAGATAAAATAAAACACTCAGGAGTTCCACAAATTCTACACTCATGG
 CAGGAACCCAGTAGGATACCCACTGGCTGGCAATTCTGAGGAAA
 ACTGGAAACAAACTTG
 TACAAAAGTTGAACCTGGCTCATCTCCATAGCCCACATGTAATGGGTACAACAAATCAA
 TTCTCCACAAGAACACGGCTTGAAGAGGATTCTCAGCTCTTGAAAGAAAATGG
 TTCTCAGCTCCGTGTCACAGACAAATTGAAACCATTGAAAGAAA
 ACATCGGTTGGATGG
 ATAAGAATTGATAAAATCAGAGTGTGGCTGCAAAGTGAAGAAAAGCTGAAACGTATG**TAAAAA**
 TTCCTCCCTGCCGGTCTGTATCTCTAATCACCACATTGAGGTTGAGTGTATT
 ACTAGAGATGGCTGTTGGCTCCA
 ACTGGAGATACTTTTCCCTCAACTCATT
 TCGCTACCATGTGTTGTCATCACAGGTGTTGCCCTGCAACGTA
 AACCCAAAGTGGTGG
 TCCCTGCCACAGAAGAATAAGTACCTTATTCTCAAAAAAAAAAAAA

FIGURE 248

MVFLPLKWSLATMSFLLSSLLALLTVSTPSWCQSTEASPKRSDGTPFPWNKIRLPEYVIPVH
 YDLLIHANLTTLFWGTTKVEITASQPTSTIILHSHHLQISRATLRKGAGERLSEEPLQVLE
 HPPQEIQIALLAPEPLLVLGPYTVVIHYAGNLSETFHGFYKSTYRTKEGELRILASTQFEPTA
 ARMAFPCFDEPAFKASFISIKIRREPRHLAISNMPLVKSVTVAEGLIEDHFDVTVKMSTYLVA
 FIISDFESVSKITKSGVKVSVYAVPDKINQADYALDAAVTLEFYEDYFSIPYPLPKQDLAA
 IPDFQSGAMENWGLTTYRESALLFDAEKSSASSKLGITVTVAHELHQWFGNLVTMEWWNDL
 WLNEGFAKFMEFVSVSVTHPELKVGDYFFGKCFDAMEVDALNSSHPVSTPVENPAQIREMFD
 DVSYDKGACILNMLREYLSADAFKSGIVQYLQKHSYKNTKNEDLWDSMASICPTDGVKGMDG
 FCSRSQHSSSSSHWHQEGVDVKTMNTWTIQRGFPLITITVRGRNVHMKQEHYMKSGDGAPD
 TGYLWHVPLTFITSKSNMVHRFLLKTVDLILPEEEWIKFNVGMNGYYIVHYEDDGWDSL
 TGLLKGTHTAVSSNDRASLINNAFQLVSIGKLSIEKALDLISLYLKHETEIMPVFQGLNELIP
 MYKLMEKRDNEVETQFKAFLIRLLRDLIDKQTWTDEGSVSEQMLRSELLLLACVHNYQPCV
 QRAEGYFRKWKESNGNLSPDVDTLAVFAVGAQSTEGWDFLYSKYQFSLSSTEKSQIEFALC
 RTQNKEKLQWLDESFKGDKIKTQEFPQILTIGRNPVGYPLAWQFLRKWNWKLVQKFELGS
 SSIAHMVMGTTNQFSTRTRLEEVKGFFSSLKENGSQLRCVQQTIETIEENIGWMDKNFDKIR
 VWLQSEKLERM

Signal peptide:

amino acids 1-34

N-glycosylation sites:

amino acids 70-74, 154-158, 414-418, 760-764, 901-905

Neutral zinc metallopeptidases, zinc-binding region signature:

amino acids 350-360

FIGURE 249

CAGCCACAGACGGGTATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCCAC
 TGCCAGGAGTGCAGGCCTGCTCTGCCAGTTGGGACAGTTCAGCATGTGTGGAAGGTGTCC
 GACCTACCCCGGAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTGGGTGCCAGGA
 CACGTTGATGCTATTGAGAGCGGACCCAAGTGAGCCTGGTGTCTCCAAGGGCTGCACGG
 AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCGGCCTCCCTGATC
 TCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT
 TTGGGCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTGTCTATGG
 AAGGCTGTCTGGAGGGACAACAGAACAGAGATCTGCCCAAGGGACCACACACTGTTATGAT
 GCCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC
 CCAGCCAGGTTGCAACCTGCTCAATGGACACAGGAAATTGGGCCGTGGTATGACTGAGA
 ACTGCAATAGGAAAGATTTCTGACCTGTCACTGGGGGACCACCAATTATGACACACGGAAAC
 TTGGCTCAAGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGCAGGT
 GTGTCAGGAGACGCTGCTCATAGATGTAGGACTCACATCAACCTGGTGGGACAAAAG
 GCTGCAGCACTGTTGGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCTCCTGG
 GTGCTTGTGCCCTCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCAGCAGCAG
 CAGCGTTCTGCTGAACCTCCCTCCCTCAAGCTGCCCTGTCCCAGGAGACCGCAGTGT
 CTACCTGTGTGCAGCCCTTGGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCAGG
 GGCGCCACTCATTGTTATGATGGGTACATTCACTCTCAGGAGGTGGCTGTCCACCAAAAT
 GAGCATTCAAGGCTGCGTGGCCAACCTCCAGCTTGTGAACCACACCAGACAAATCG
 GGATCTCTGCGCGTGAGAAGCGTATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGT
 GGGGCTGAGGGCTGGAGTCTCTCACTTGGGGGTGGGCTGGCACTGGCCCCAGCGCTGTG
 GTGGGGAGTGGTTGCCCTCCTGCTTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGA
 CCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGCCCTGGACACCAGATTCTTC
 CCATTCTGTCCATGAATCATCTCCCCACACACAATCATTCACTACTCACCTAACAGCA
 AACACTGGGAGAGCCTGGAGCATCCGGACTTGCCTATGGGAGAGGGACGCTGGAGGAGTG
 GCTGCATGTATCTGATAATACAGACCCCTGTCCTTCA

FIGURE 250

MSAVLLLALLGFILPLPGVQALLCQFGTVQHVKVSDLPRQWTPKNTCDSGLGCQDTLMLI
ESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLWAPQP
PADPGSLRCPVCLSMEGCLEGTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCMPQPGCN
LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTSNTEMCEVGQVCQETL
LLIDVGLTSTLVGTLKGCVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCNSASSSVLLN
SLPPQAAPVPGDRQCPTCVQPLGTCSSGS PRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGC
VAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGAEGLESLTWGVGLALAPALWWGVVC

PSC

FIGURE 251

CGCACGGGCAGGACGCCCGTTCGCCTAGCGCGTGCAGGAGTTGGTGTCCCTGCCTGCGCT
CAGG**ATG**AGGGGAATCTGGCCCTGGTGGCGTTCAATCAGCCTGGCCTCTGTCACTGCTG
CCATCTGGACATCCTCAGCCGGCTGGCGATGACGCCTGCTCTGTCAGATCCTCGTCCCTGG
CCTCAAAGGGATGCGGGAGAGAAGGGAGACAAAGGCACCCCCGGACGGCCTGGAAGAGTCG
GCCACCGGGAGAAAAAGGAGACATGGGGACAAAGGACAGAAAAGGCAGTGTGGTCGTCA
GGAAAAATTGGTCCCATTGGCTCTAAAGGTGAGAAAGGAGATTCCGGTGACATAGGACCCCC
TGGTCCTAATGGAGAACCAAGGCCTCCCATGTGAGTGCAGCCAGCTGCGCAAGGCCATCGGG
AGATGGACAACCAGGTCTCTCAGTGACCAGCGAGCTCAAGTCATCAAGAATGCTGTCGCC
GGTGTGCGCGAGACGGAGAGCAAGATCTACCTGCTGGTGAAGGAGGAGAACGCGTACGCC
CGCCAGCTGCTGCCAGGGCCCGGGGCACGCTGAGCATGCCAAGGACGAGGCTGCCA
ATGGCCTGATGCCGCATACCTGGCGCAAGCCGGCTGGCCGTGTCTTCATGGCATCAAC
GACCTGGAGAAGGAGGGCGCTTCGTGTACTCTGACCACTCCCCATGCGGACCTTCAACAA
GTGGCGCAGCGGTGAGCCAACAATGCCTACGACGAGGAGCTGCGTGGAGATGGTGGCCT
CGGGCGGCTGGAACGACGTGGCCTGCCACACCACCATGTACTTCATGTGTGAGTTGACAAG
GAGAACATG**TGA**GCCTCAGGCTGGGCTGCCATTGGGGCCCCACATGTCCCTGCAGGGTT
GGCAGGGACAGAGCCCAGACCATGGTGCCAGCCAGGGAGCTGTCCTGTGAAGGGTGGAG
GCTCACTGAGTAGAGGGCTGTTGTCTAAACTGAGAAAATGCCATGCTTAAGAGGAAAATG
AAAGTGTTCCTGGGTGCTGTCTGAAGAAGCAGAGTTCAATTACCTGTATTGTAGCCCCA
ATGTCATTATGTAATTATTACCCAGAATTGCTCTTCCATAAGCTTGTGCCTTGTCCAAGC
TATACAATAAAATCTTAAAGTAGTGCAGTAGTTAAAGCTTGTGCCTTGTCCAAGC

FIGURE 252

MRGNLALVGVLISLAFLSLLPSGHQPAGDDACSVQILVPGLKGDAGEKGDKGAPGRPGRVG
PTGEKGDMDKGQKGSGVGRHGKIGPIGSKGEKGDSGDIGPPGPNGEPGLPCECSQLRKAIGE
MDNQVSQLTSELKEFIKNAVAGVRETESKIYLLVKEEPRYADAQLSCQGRGGTLSMPKDEAAN
GLMAAYLAQAGLARVFIGINDLEKEGAFVYSDHSPMRTFNKWRSGEPNNADEEDCVELVAS
GGWNDVACHTTMYFMCEFDFKENM

FIGURE 253

AGTGACTGCAGCCTTCCTAGATCCCCTCCACTCGTTCTCTCTTGCAGGAGCACCGGCAG
CACCACTGTGTGAGGGGAGCAGGCAGCGGTCTAGCCAGTCCTGATCCTGCCAGACCACC
CAGCCCCCGGCACAGAGCTGCTCACAGGCACC**ATG**AGGATCATGCTGCTATTACAGCCAT
CCTGGCCTTCAGCCTAGCTCAGAGCTTGGGCTGTCTGTAAGGAGCCACAGGAGGAGGTGG
TTCCTGGCGGGGGCCGCAGCAAGAGGGATCCAGATCTCTACCAGCTGCTCCAGAGACTCTC
AAAAGCCACTCATCTGGAGGGATTGCTCAAAGCCTGAGCCAGGCTAGCACAGATCCTAA
GGAATCAACATCTCCCAGAAACGTGACATGCATGACTCTTGTGGACTTATGGGAAAGA
GGAGCGTCCAGCCAGAGGGAAAGACAGGACCTTACCTTCAGTGAGGTTCCCTCGGCC
CTTCATCCCAATCAGCTGGATCCACAGGAAAGTCTCCCTGGAACAGAGGAGCAGAGACC
TTT**TAA**ACTCTCCTACGGATGTGAATCAAGAGAACGTCCCCAGCTTGGCATCCTCAAGT
ATCCCCCGAGAGCAGAATAGGTACTCCACTCCGGACTCCTGGACTGCATTAGGAAGACCTC
TTTCCCTGTCCAATCCCCAGGTGCGCACGCTCCTGTTACCTGACCCTGGTGTGGAAACTGCA
AACATTCTTGCTTGACTCCTCTCCATCTTCTACCTGACCCTGGTGTGGAAACTGCA
TAGTGAATATCCCCAACCCAAATGGCATTGACTGTAGAATACCTAGAGTCTGTAGTGT
CCTACATTAAAAATAATGTCTCTCTATTCCCTCAACAATAAAGGATTTGCATATGAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 254

MRIMLLFTAILAFSLAQSGAVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGLLK
ALSQASTDPKESTSPEKRDMDFFVGLMGKRSVQPEGKTGPFLPSVRVPRPLHPNQLGSTGK
SSLGTEEQRPL

Important features:

Signal peptide:

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 36-45

N-myristoylation site.

amino acids 33-39, 59-65

Amidation site.

amino acids 90-94

Leucine zipper pattern.

amino acids 43-65

Tachykinin family signature.

amino acids 86-92

FIGURE 255

GGGCGTCTCCGGCTGCTCCTATTGAGCTGTCTGCTCGCTGTGCCCGCTGTGCCTGCTGTGCC
 CGCGCTGTCGCCGCTGCTACCGCGTCTGCTGGACGCCGGAGACGCCAGCGAGCTGGTATTG
 GAGCCCTGCCGGAGAGCTCAAGGCCAGCTCTGCCAGGAGGCCAGGCTGCCCGTGAGTC
 CCATAGTTGCTGCAGGAGTGGAGCC**ATG**AGCTGCGTCTGGTGTCACTCCCTGGGGC
 TGCTGTCCTGGTCTGCCGATCCAAAGGCTACCTCCTGCCAACGTCACTCTTAGAGGAG
 CTGCTCAGCAAATACCAGCACAAACGAGTCTCACTCCGGTCCGCAGAGCCATCCCCAGGGA
 GGACAAGGAGGAGATCCTCATGCTGCACAACAAGCTCGGGCCAGGTGCAGCCTCAGGCCT
 CCAACATGGAGTACATGGTAGCGCCGGCTCCGGCCGCAGAGGCTGGCACCGGGGTGGGGC
 CTGGGCCACCAGCCTGCTCTGTTCCCCAGCCAGCTCTGTTCCCCAGCCAGTGCCTGTGATGG
 CTGGCTCAGGGTCTCCTCTGGCAGGGGAGGATCCGGCTCTGTTCTGTTCTGTTGTTGTT
 TTGAGACAGGGTCTCACTCTGCCACTGACGCTGGAGTGCAATGGCACAATCGTCATGCCCTG
AAACCT**TAG**ACTCCCAGGGTTAACGATCCTGCTCAGCCTCCAAGTAGCTGGAACACTACAG
 GCATGCACCATGGTCCCAGCTAGATTTAAATATTTGTGGAGATGGGGTCTGCTACGT
 TGCCCAGGCTGGTCTTGAACTCCTAGGCTCAAGCAATCCTCCTGCCCTCAGCCTCTCAAAGTG
 CTAGGATTATAGGCATGAGTCACCCGTCTGGCTCTGGCTCTGTTCTAACATTCTGCCAAA
 ACAACACACGTGGGTTCCCTGTGCAGAGCCTGCCCTGCTTCATGTCACTCTGGTAGC
 TCCACTGGAACACAGCTCTCAGCCTTCCCACCTGGAGGCAGAGTGGGAGGGGCCAGGG
 CTGGGCTTGCTGATGCTGATCTCAGCTGTGCCACACGCTAGCTGCACCACCCGTACTTCTC
 CTTAGCCGTGTGAGCCTCACTTCCACTGGAGAGTCCTCCTCGGTGGCTGCCATGACT
 GTGAGATAAGTCGAGGCTGTGAAGGGCCGGCACAGACTGACCTGCCCTCCAACCCCTAGG
 CTTTGCTAACCGGAAAGGAGCTAACGGTACAGAAGACAGCCAAGGTCAACCCTCCGGGT
 GATTGTGATGGGTGTTCCAGGTGTGGTTGGCGATGCTGACTTGACCCCAAGCTCCAGTG
 TGGAAACTCCCTCCTGGCTGGTTCCAGAAGTACAGAGGAATGGACCAAGTCTCCAGG
 GTCCCTCCTGCCACCAACGGGAGCCTCCACCTGGCATCCGTAGCTATGAATGGCTT
 TTTAAACAAACCCACGTCCCAGCCTGGTAACATGGTAAAGCCCCGTCTACAAAAAAATC
 CAAGTAGCCGGCATGGTGGTGCACCTGTAGTCCAGCTGCAGTGGACTGAGGTGGAG
 GTGGAGGTGGGGGTGGGAGCTGAGGAAGGAGGATCGCTGAGCCTGGGAAGTCGAGGCTGC
 AGTGAGCTGAGATTGCACCACTGCACTCCAGCCTGGGTACAGAGCAAGACCCTGTCTAAAAA

FIGURE 256

MSCVLGGVIPLGLLFLVCGSQGYLLPNVTILLELLSKYQHNESHSRVRAIPREDKEEILML
HNKLRGQVQPQASNMEYMVSAGSGRRGWHRGGLGHQPALFSQLCSPASACDGWLKVSSGR
GGSRLCSVLFVCFETGSHSATDAGVQWHNRHALKP

Important features:

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 27-31, 41-45

N-myristoylation site.

amino acids 126-132, 140-146

Amidation site.

amino acids 85-89

FIGURE 257

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCATCCCAGGAGCGCAGTGGCCACTATGGG
GTCTGGGCTGCCCTTGTCCCTCCTGGACCCCTCCTGGCAGCTCACATGGAACAGGGCCGG
GTATGACTTGCAACTGAAGCTGAAGGAGTCTTGACAAATTCCCTCATGAGTCCAGC
TTCCTGGAATTGCTTGAAAAGCTCTGCCTCCTCCATCTCCCTTCAGGGACCAGCGTCAC
CCTCCACCATGCAAGATCTAACACCATGTTGTCTGCAACACATGACAGCCATTGAAGCCTG
TGTCCCTCTGGCCCGGGCTTTGGCCGGGATGCAGGAGGCAGGCCCGACCCTGTCTT
CAGCAGGCCACCCCTCCTGAGTGGCAATAAATAAATTCGGTATGCTG

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FIGURE 258

MGSGPLVLLTLLGSSHGTGPGMTLQLKLKESFLTNSSYESSFLELLEKLCLLHLPSGTS
VTLLHARSQHHVVVCNT

FIGURE 259

AATTGTATCTGTGTAATGTTAAAACAAACGAAATAAGAAGGAAAAACTTCTGAGTT
CAAAAACAACAGACTAGTACTCTAAAGAACACTCTTAAAACAATTAACTGTTAGGATTGCAGT
TATGATTGGATATTATTAATTCTGTTCTGATGTGGGTTCCACTGTGTTCTGTGTC
TATTAATATTTACCATTGCAGAACGCTTCATTCACTGTTGAAAATGAATGCTTAGTGGATCTG
TGCCTCTTACGCATATGTTACAAATTATCTGGAGTCTTAATCAATGCAGAGTTCCCCTCCC
CTCCGATTGTTCTAAA**TAA**TTGAAAGATGTCTGCTGTGGAAAAAGGCATGTATTAAATCTG
TATGATTCTCAACCATCTTAGTTGGAAAGGTCTTGAAAGCCAATGGAAATACTTTTT
TTTCTTGGCACTAATCAAGTGAGTGTACCTTTCACTTAGTAGGATGTGTTACGCTA
GTAAAATAGAAACCTGTGTTATTCTCAGGTATTTAGAAACAACAGCCATCTTTATTT
ATGTGTGTGTTCTTGGCTGTATTCAAATTATATTTGGGCTATCAAATATTACTTCAT
TCAATATAAAACAATAGTAGAAGTTGTTACTTAGATATGCTTCTAGTTGCATTTCTC
AGCCTATGTAAGACTACTTGTGAAATGCCTTGAAATTACAGTACTGTCTCTACTA
TCTTCAGATTACTTGATTCAAATAACCAATTATGTTGTAATTGATATTAATAAAACCAGA
ATAAAAGTTCATATCTACCC

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FIGURE 260

MIGYYLILFLMWGSSTVFCVLLIFTIAEASFVENECLVDLCLLRIC^YKLSGV^NQCRVPLP
SDCSK

Important features:

Signal peptide:

amino acids 1-29

FIGURE 261

GAGGAGTTGCCACAGCAGCGGATAGAGCAGGAGAGCACCACCGGAGCCCTTGAGACATCCTT
 GAGAAGAGCCACAGCATAAGAGACTGCCCTGCTTGGTGTTCAGGATGATGGTGGCCCTT
 CGAGGAGCTCTGCATTGCTGGTCTGTCCTTGCAAGCTTCTGCCCGGCCAGTGTAC
 CCAGGACCCAGCCATGGCATTACATCTACCGCGCTTCAGTCTGGAGCAAGGGCTGG
 AAAAATGTACCCAAGCAACGAGGGCATACATTCAAGAATTCAAGAGTTCTCAAAAAATATA
 TCTGTATGCTGGGAAGATGTCAGACCTACACAAGTGAGTACAAGAGTGCACTGGGTAACCT
 GGCACGTGAGAGTTGAACGTGCCAACGGGAGATTGACTACATAACATACCTCGAGAGGGCTG
 ACGAGTGCATCGTATCAGAGGAAAGACACTGGCAGAAATGTTGCTCCAAGAAGCTGAAGAA
 GAGAAAAGATCCGGACTGCTGAATGCAAGCTGTGACAAACATGCTGATGGCATAAAGTC
 TTTGAAAATAGTGAAGAAGATGATGGACACATGGCTTGGATGAAAGATGCTGTCTATA
 ACTCTCCAAGGGTGTACTTATTAAATTGGATCCAGAAACAAACATGTTGGAAATTGCAAAC
 ATACGGGCATTATGGAGGATAACACCAAGCCAGCTCCCCGGAAGCAAATCTAACACTTTC
 CTGGCAGGGAAAGGCCAAGTGAATCTACAAAGGTTCTATTCTATAACCAAGCAACTT
 CTAATGAGATAATCAAATATAACCTGCAGAAGAGGACTGTGGAAGATGCAATGCTGCCA
 GGAGGGTAGGGCGAGCATTGGTTACCAAGCTCCCCCTCAACTTACATTGACCTGGCTGT
 GGATGAGCATGGCTCTGGCCATCCACTCTGGGCCAGGCACCCATAGCCATTGGTCTCA
 CAAAGATTGAGCCGGCACACTGGGAGTGGAGCATGGATACCCATGCAAGAGCAG
 GATGCTGAAGCCTATTCTCTTGTGTGGGTTCTATGTTGCTACAGTACTGGGGCCA
 GGGCCCTCATCGCATCCTGCATCTATGATCCACTGGCACTATCAGTGAGGAGGACTTGC
 CCAACTTGTCTCCCCAAGAGACCAAGAAGTCACTCCATGATCCATTACAACCCCAGAGAT
 AAGCAGCTCTATGCCTGGAATGAAGGAAACCAGATCATTACAAACTCCAGACAAAGAGAAA
 GCTGCCTCTGAAGTAAATGCACTACAGCTGTGAGAAAGAGCACTGTGGCTTGGCAGCTGTC
 TACAGGACAGTGAGGCTATAGCCCCCTCACAATATAGTATCCCTTAATCACACACAGGAAG
 AGTGTGTAGAAGTGGAAATACGTATGCCTCTTCCAAATGTCACTGCCTTAGGTATCTTC
 CAAGAGCTTAGATGAGAGCATATCATCAGGAAAGTTCAACAATGTCCATTACTCCCCAAA
 CCTCCTGGCTCTCAAGGATGACCACATTCTGATACAGCCTACTCAAGCCTTTGTCTTACT
 GCTCCCCAGCATTACTGTAACTCTGCCATCTCCCTCCACAATTAGAGTTGATGCCAGC
 CCCTAATATTCAACCCTGGCTTCTCTCTCCCTGGCCTTGTGAAGCTCTCCCTTT
 CAAATGTCTATTGATATTCTCCATTTCACTGCCAACTAAAATACTATTAAATATTCTT
 CTTTCTTTCTTTTTGAGACAAGGTCTCACTATGTTGCCAGGTGGCTCAAACCTCC
 AGAGCTCAAGAGATCCTCCTGCCCTAGCCTCCTAAGTACCTGGGATTACAGGCATGTGCCAC
 CACACTGGCTAAAATACTATTCTTATTGAGGTTAACCTCTATTCCCTAGCCCTGTC
 CTTCCACTAAGCTGGTAGATGTAATAATAAAAGTAAAAATATTAAACATTGAATATCGCTT
 CCAGGTGTGGAGTGTTCACATCATTGAATTCTCGTTCACCTTGTGAAACATGCACAAG
 TCTTACAGCTGTCACTTAGAGTTAGGTGAGTAACACAATTACAAAGTGAAAGATACAGC
 TAGAAAATACTACAAATCCCATTGCCAAGGAAGCATCAAATACGTATGTT
 TGTTCACCTACTCTTATAGTCAATGCGTTCATGTTCAAGCTTCAAAATAATAGTCTGCCC
 TTAGGCCAGTTCATGCTGCACAAGACCTTCAATAGGCCTTCAAATGATAATTCCCTCC
 AGAAAACCAAGTCAAGGGTGAGGACCCAACTTAGCCTCTTGCTGTCTGCTGT
 TTCTCTTTCTGCTTAAATTCAATAAAAGTGACACTGAGCAAAAAAAAAAAAAA

FIGURE 262

MMVALRGASALLVLFLAAFLPPPQCTQDPAMVHYIYQRFRVLEQGLEKCTQATRAYIQEFQE
FSKNISVMLGRCQTYTSEYKSAVGNLALRVERAQRREIDYIQLREADECIVSEDKTLAEMLL
QEAEKKIRTLNASCDNMLMGIKSLKIVKKMDTHGSWMKDADVNSPKVYLLIGSRNNTV
WEFANIRAFMEDNTKPAPRKQILTLSWQGTGQVIYKGFLFFHNQATSNEIIKYNLQKRTVED
RMLLPGGVGRALVYQHSPSTYIDLAVDEHGLWAIHSGPGTHSHLVLTKEPGTLGVEHSWDT
PCRSQDAEASFLLCGVLYVVYSTGGQGPHRITCIYDPLGTISEEDLPNLFFPKRPRSHSMIH
YNPRDKQLYAWNENQIIFYKLQTKRKLPLK

FIGURE 263

GGGCGCCCGCGTACTCACTAGCTGAGGTGGCAGTGGTTCCACCAAC **ATG**GAGCTCTCGCAGA
 TGTGCGGAGCTCATGGGCATGGCTGCGTGGTGTGCTGGCCTGCTGGCCCTGATGGCGACGGCGGGCG
 GTAGCGCGGGGGTGGCTGCGCGGGGGAGGGAGAGGGAGCAGGCCGGCCCGCTGCCAAAAAGC
 AAATGGATTTCACCTGACAAATCTCGGGATCCAAGAACAGAAACAAATATCAGCGGATTC
 GGAAGGAGAACGCTCAACAACACAACCTCACCCACCGCCTCTGGCTGCAGCTGAAGAGC
 CACAGCGGGAACATATCTGCATGGACTTTAGCAGCAATGGCAAATACCTGGCTACCTGTGC
 AGATGATCGCACCACCGCATCTGGAGCACCAAGGACTTCCTGCAGCGAGAGCACCGCAGCA
 TGAGAGCCAACGTGGAGCTGGACCACGCCACCCCTGGTGCCTCAGCCCTGACTGCAGAGCC
 TTCATCGTCTGGCTGGCCAACGGGGACACCCCTCCGTGTCTCAAGATGACCAAGCGGGAGGA
 TGGGGCTACACCTCACAGCCACCCCAGAGGACTTCCTAAAAGCACAAGGCCTGTCA
 TCGACATTGGCATTGCTAACACAGGGAAAGTTATCATGACTGCCTCCAGTGACACCAGTC
 CTCATCTGGAGCCTGAAGGGTCAAGTGCTGTCTACCACCAACACCAACCAGATGAACAAACAC
 ACACGCTGCTGTATCTCCCTGTGGCAGATTGTAGCCTCGTGTGGCTCACCCAGATGTGA
 AGGTTGGGAAGTCTGCTTGGAAAGAAGGGGGAGTTCCAGGAGGTGGTGCAGCCTCGAA
 CTAAAGGCCACTCCGGCTGTGCACTCGTTGCTTCTCAACGACTCACGGAGGATGGC
 TTCTGTCTCCAAGGATGGTACATGGAAACTGTGGGACACAGATGTGGAATAAAGAAGAAGC
 AGGACCCCTACTTGCTGAAGACAGGCCAGGTCTGGCCTTGAAGAGGCGGGTGCAGCCTG
 CTGGCCCTCTCCCCAACGCCAGGTCTGGCCTTGAAGAGGCGGGTGCAGCCTG
 CAATACCCGGCGGGCGAGAAGGAGGAGTGCTTGAAGAGGCGGGTGCAGCCTG
 ACTTGCTCTTGACATCACTGGCCCTTCTGGCCTCTGTGGGACCGGGCGGTGCAGCCTG
 TTTCACAACACTCCTGGCACCGAGCCATGGTGGAGGAGATGCAGGGCACCTGAAGCAGG
 CTCCAACGAGAGCACCGCCAGAGGCTGCAGCAGCAGCTGACCCAGGCCAACAGAGACCC
 AGAGCCTGGGTGCCCTGAAGAAG**TGA**CTGGGAGGGCCCGCGCAGAGGATTGAGGAGGAG
 GGATCTGGCTCTCATGGCACTGCTGCCATCTTCTCCATTGAAACTACTCTGTCTACTT
 AGTCTCCTGGTTTCTTACTGGTGGCCCTGCTTCTTCCATTGAAACTACTCTGTCTACTT
 AGGTCTCTCTCTTGCTGGCTGTGACTCCTCCCTGACTAGTGGCAAGGTGCTTCTTC
 CTCCCAGGCCAGTGGTGGAACTGTCCCCACCTGGCACTGAGGAGAATGGTAGAGAGGAG
 AGGAGAGAGAGAGAGAATGTGATTTGGCCTTGTGGCAGCACATCCTCACACCCAAAGAAG
 TTTGTAATGTTCCAGAACACCTAGAGAACACCTGAGTACTAAGCAGCAGTTGCAAGGA
 TGGGAGACTGGGATAGCTCCCACAGAACTGTGTTCCATCAAAAGACACTAAGGGATT
 TCCTCTGGGCCCTCAGTTCTATTGTAAGATGGAGAATAATCCTCTGTGAACCTTGCA
 AAGATGATATGAGGCTAACAGAAATATCAAGTCCCCAGGTCTGGAGAAAGAAAGAGT
 AGTACTATTGTCCAATGTCAAGAACAGTGGAAAAGTGGGAACCAAGTGTGCTTGAACCAAA
 TTAGAAACACATTCTGGAGGCAAGGCTTCTGGACTTGATCATACATTATATGGT
 TGGGACTTCTCTTCAGGAGATGATATCTGTGTTAAGGAGACCTCTTCAGTTCAAG
 TTCATCAGATATTGAGTGCCCACCTGTGCCAAATAATGAGCTGGGATTAAAAAAA
 AA

FIGURE 264

MELSQMSELMGLSVLLGILALMATAAVARGWLRA GEERSGRPACQKANGFPPDKSSGSKKQK
QYQRIRKEKPQQHNFTHRLLAAALKSHSGNISCMDFSSNGKYLATCADDRTIRIWSTKDFLQ
REHRSMRANVELDHA TLVRFSPDCRAFIVWLANGDTLRFKMTKREDGGYTFTATPEDFPKK
HKAPVIDIGIANTGKFIMTASSDTTVLIWSLKGQVLSTINTNQMNNTHAAVSPCGRFVASC
FTP DVKVWEVCFGKKGEFQEVVRAFELKGHSAAVHSFAFSNDSRRMASVSKDGTWKLWDTDV
EYKKKQDPYLLKTGRFEAAAGAAPCRLALSPNAQVLALASGSSIHLYNTRRGEKEECFERVH
GECIANLSFDITGRFLASCGDRAVRLFHNTPGH RAMVEEMQGHLKRASNESTRQLQQQLTQ
AQETLKSLGALKK

Important features:

Signal peptide:

amino acids 1-25

N-glycosylation site.

amino acids 76-80, 92-96, 231-235, 289-293, 378-382, 421-425

Beta-transducin family Trp-Asp repeat protein.

amino acids 30-47, 105-118, 107-119, 203-216, 205-217, 296-308

FIGURE 265

TGGCCTCCCCAGCTGCCAGGCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAACGAGG
 CAGTGTTCGCCTCACCCCAAGTGACC**ATG**AGAGGGGCCACGCGAGTCTCAATCATGCTCC
 TCCTAGTAACTGTGCTGACTGTGCTGTGATCACAGGGGCCTGTGAGCGGGATGTCCAGTGT
 GGGCAGGCACCTGCTGCCATCAGCCTGTGGCTCGAGGGCTGCCAGGATGTGCCACCCGCT
 GGGCGGGAAAGGCGAGGGAGTGCCACCCCGGCAGCCACAAGGCTCCCTTCAGGAAACGCA
 AGCACCACACCTGCTCCTGCTTGCCAACCTGCTGTGCTCCAGGTTCCGGACGGCAGGTAC
 CGCTGCTCCATGGACTTGAAGAACATCAATT**TAG**GCGCTTGCCTGGTCTCAGGATAACCA
 CCATCCTTCTGAGCACAGCCTGGATTTATTCTGCCATGAAACCCAGCTCCATGAC
 TCTCCCAGTCCCTACACTGACTACCCCTGATCTCTTGTCTAGTACGCACATATGCACACAG
 GCAGACATACCTCCATCATGACATGGTCCCCAGGCTGCCAGGATGTCACAGCTTGAGG
 CTGTGGTGTGAAAGGTGCCAGCCTGGTTCTTCCCTGCTCAGGCTGCCAGAGAGGTGGTA
 AATGGCAGAAAGGACATTCCCCCTCCCCCAGGTGACCTGCTCTTCCCTGGCCCTG
 CCCCTCTCCCCACATGTATCCCTGGTCTGAATTAGACATTCCCTGGCACAGGCTCTGGGT
 GCATTGCTCAGAGTCCCAGGTCCCTGCCCTGACCCCTCAGGCCCTCACGTGAGGTCTGTGAGG
 ACCAATTGTGGTAGTTCATCTCCCTCGATTGGTTAACCTCTTAGTTTCAGACCACAGAC
 TCAAGATTGGCTCTTCCCAGAGGGCAGCAGACAGTCACCCCAAGGCAGGTGTAGGGAGCCC
 GGGAGGCCAATCAGCCCCCTGAAGACTCTGGTCCAGTCAGCCTGTGGCTTGCCCTGTGA
 CCTGTGACCTCTGCCAGAATTGTCATGCCCTGAGGCCCTCTTACACACTTACCA
 TAACCACGTAGCCCCCAATTCCCACAGCTTTCCATTAAATGCAAATGGTGGTCAA
 TCTAATCTGATATTGACATATTAGAAGGCAATTAGGGTGTTCCTAAACAACCTCTTCCA
 AGGATCAGCCCTGAGAGCAGGTGGTACTTGAGGGAGGGCAGTCCTGTCCAGATTGGGG
 TGGGAGCAAGGGACAGGGAGCAGGGCAGGGCTGAAAGGGGACTGATTCA
 GACACCAGGGAGG
 CAACTACACACCAACATGCTGGCTTAGAATAAAAGCACCAACTGAAAAAA

FIGURE 266

MRGATRVSIMLLLTVSDCAVITGACERDVQCGAGTCCAISLWLRLRMCTPLGREGEECHP
GSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCSDLKNINF

Signal peptide:

amino acids 1-19

Tyrosine kinase phosphorylation site:

amino acids 88-95

N-myristoylation sites:

amino acids 33-39, 35-41, 46-52

FIGURE 267

AGCGCCGGGCGTCGGGCGGTAAAAGGCCGGCAGAAGGGAGGCACTTGAGAA**ATG**TCTTC
CTCCAGGACCAAGTTCTCACCATGGGATGTGGTCCATTGGTGCAGGAGCCCTGGGGC
TGCTGCCTTGGCATTGCTGCTGCCAACACAGACGTGTTCTGTCCAAGCCCCAGAAAGCGG
CCCTGGAGTACCTGGAGGATATAGACCTGAAAACACTGGAGAAGGAACCAAGGACTTCAA
GCAAAGGAGCTATGGAAAAAAATGGAGCTGTGATTATGCCGTGCGGAGGCCAGGCTGTT
CCTCTGTCGAGAGGAAGCTGCGGATCTGTCCTCCCTGAAAAGCATGTTGGACCAGCTGGCG
TCCCCCTCATGCAGTGGTAAAGGAGCACATCAGGACTGAAGTGAAGGATTCCAGCCTTAT
TTCAAAGGAGAAATCTCCTGGATGAAAAGAAAAAGTTCTATGGTCCACAAAGGCCAGAGAT
GATGTTATGGATTATCCGTCTGGAGTGTGGTACAACCTCTCCAGCCTGGAACGGAG
GCTTCTCTGAAACCTGGAAGGAGAAGGCTTCATCCTGGGGAGTTTGTGGTGGGATCA
GGAAAGCAGGGCATTCTCTTGAGCACCGAGAAAAAGAATTGGAGACAAAGTAAACCTACT
TTCTGTTCTGGAAGCTGCTAACGATGATCAAACACAGACTTGGCCTCAGAGAAAAAA**TGA**
TGTGTGAAACTGCCAGCTCAGGGATAACCAGGGACATTCACCTGTGTTATGGATGTATT
GTTTCCACTCGTGTCCCTAACGGAGTGAGAAACCCATTATACTCTACTCTCAGTATGGATTA
TTAATGTATTTAATATTCTGTTAGGCCACTAACGGCAAAATAGCCCCAAACAAGACTGA
CAAAATCTGAAAACTAATGAGGATTATTAAGCTAACCTGGAAATAGGAGGCTTAAAA
TTGACTGCCAGGCTGGGTGCAGTGGCTCACACCTGTAATCCCAGCAGTTGGAGGCCAAGG
TGAGCAAGTCACTGAGGTCGGAGTTCGAGACCAGCCTGAGCAACATGGCGAAACCCCGTC
TCTACTAAAAATACAAAATCACCCGGGTGTGGTGGCAGGCACCTGTAGTCCAGCTACCCG
GGAGGCTGAGGCAGGAGAATCACTGAACCTGGAGGTGGAGGTTGCCGTGAGCTGAGATCA
CACCACTGTATTCCAGCCTGGGTGACTGAGACTCTAACTAA

FIGURE 268

MSFLQDPSFFTGMWSIGAGALGAAALALLANTDVFLSKPQKALEYLEDIDLKTLEKEPR
TFKAKELWEKNGAVIMAVRRPGCFLCREEAADLSSLKSMLDQLGVPLYAVVKEHIRTEVKDF
QPYFKGEIFLDEKKKFYGPQRKMMFMGFIRLGWYNFFRAWNGGFSGNLEGEGFILGGVFV
VGSGKQGILLEHREKEFGDKVNLLSVLEAAKMIKPQTLASEKK

FIGURE 269

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCG
GGCCAGGTGCCCGTCGCAGGTGCCCTGCCGGAGATGCGGTAGGAGGGCGAGCGCGAGA
AGCCCCTTCCTCGCGCTGCCAACCGCCACCCAGCCCATGCGAACCCGGCTGGGCTG
CTTCTGGCGCTGGGCTGCCGTTCTGCTGGCCCGCTGGGGCGAGCCTGGGGCAAATACA
GACCACTTCTGCAAATGAGAAATAGCACTGTTGCCTCATCCACCAGCTCCAGCTCCGATG
GCAACCTCGTCCCGAACGCATCACTGCTATCATCGTGGCTTCTCCCTCTGGCTGCCTG
CTCCTGGCTGTGGGCTGGCACTGTTGGTGCAGCTTCGGAGAACGGCAGACGGAGGG
CACCTACCGGCCAGTAGCGAGGAGCAGTTCTCCATGCAGCCGAGGCCGGCCCTCAGG
ACTCCAAGGAGACGGTGCAGGGCTGCCATCTAGGTCCCTCTCCTGCATCTGTCTCC
CTTCATTGCTGTGACCTTGGGAAAGGCAGTGCCCTCTGGCAGTCAGATCCACCCAG
TGCTTAATAGCAGGAAGAAGGTACTTCAAAGACTCTGCCCTGAGGTCAAGAGAGGATGGG
GCTATTCACTTTATATATTATAAAAATTAGTAGTGAGATGTAAAAAAAAAAAAAAA

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FIGURE 270

MANPGLGLLLALGLPFLARWGRAWGQIQTTSANENSTVLPSSSSDGTLRPEAITAIIV
VFSLLAALLLAVGLALLVRKLREKRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

FIGURE 271

AATATATCATCTATTCATTAATCAATAATGTATTCTTTATTCCAATAACATTTGGGTT
TTGGGATTTAATTTCAAACACAGCAGA**ATG**ACATTTTCTGTCACTATTATTATTGTTG
GTATGTGAAGCTATTGGAGATCCAATTCAAGAACACACATTGGAGAATGGCTACTTCT
ATCAAGAAATAAAGAGAACACAGTCACCCACACAATCATCTTAGAAGACAGTGTGACTC
CTACCAAAGCTGTCAAAACCACAGGCAGGGCATAGTTAAGGACGGAATCTGACTCAAGA
GGGTTAATTCTTGGTGCTGAAGCCTGGGCAGGGGTGTAAAGAAAAACACT**TAG**ATTCAATG
ATTGTAAATTAAAGGCAAATACACATATTAGTATTACCTTAGTGTAAATGTATCCCTGTCATA
TATACAATAAGGTGAAATTATAAGTACCTATGCAGTTGGCTGGACAGTTCTAAATTGGACT
TTATTAATTTAAAATCAGTAACTGATTACTGGCTATGTGCTTAGATCTACAGGAGA
TCATATAATTGATACAATAAAAGAAAAGTGTCTCTCCCTACAGAATTGACATTTAA
ATGCGATACAGTTAGAATAGGAAATATGACATTAGAAAGGAAGAATGACAGGGAGAAAGGAA
AGAAGGGAAAATGTTGCCAAGGAAAAAA

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FIGURE 272

MTFFLSLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSOPTQSSLEDSVTPTKAVKTTGK
GIVKGRNLDSRGLLIGAEAWGRGVKKNT

FIGURE 273

GCCAGGAATAACTAGAGAGGAACAA**ATG**GGGTTATT CAGAGGTTTCTCTTAGTTCT
 GTGCCTGCTGCACCAGTC AATAC TCCCTCATTAAGCTGAATAATAATGGCTTGAGATA
 TTGT CATT GTT ATAGATCCTAGTGTGCCAGAAGATGAAAAAATAATTGAACAAATAGAGGAT
 ATGGT GACTACAGCTCTACGTACCTGTTGAAGCCACAGAAAAAGATT TTTCAAAAA
 TGTATCTATATTAAATTCCCTGAGAATTGGAAGGAAAATCCTCAGTACAAAAGGCCAAAACATG
 AAAACCATAAACATGCTGATGTTAGTTGCACCACTACACTCCCAGGTAGAGATGAACCA
 TACACCAAGCAGTTCACAGAATGTGGAGAGAAAGGCGAACATCATTCTACCCCTGACCT
 TCTACTGGAAAAAAACAAAATGAATATGGACCACCCAGGCAA ACTGTTGTCCATGAGTGGG
 CTCACCTCCGGTGGGGAGTGTGAGTACAATGAAGATCAGCCTTCTACCGTGCTAAG
 TCAAAAAAAATCGAACAAACAGGTGTCAGGTATCTCTGGTAGAAATAGAGTTATAA
 GTGTCAGGAGGGCAGCTGTCTTAGTAGAGCATGCAGAATTGATTCTACAACAAAATGTATG
 GAAAAGATTGTCAATTCTTCTGATAAAGTACAACACAGAAAAAGCATCCATAATGTTATG
 CAAAGTATTGATCTGTTGAATTGTAAACGAAAAACCCATAATCAAGAAGCTCCAAG
 CCTACAAAACATAAAGTCAATT TAGAAGTACATGGGAGGTGATTAGCAATTCTGAGGATT
 TTAAAAACACCATACCCATGGTGACACCACCTCCACCTGTCTTCATTGCTGAAGATC
 AGTCAAAGAATTGTGCTTAGTTCTGATAAGTCTGGAGCATGGGGGTAAAGGACCGCT
 AAATCGAATGAATCAAGCAGAAAACATTCTGCTGCTGAGACTGTTGAAAATGGATCCTGGG
 TGGGGATGGTTCACTTGATAGTACTGCCACTATTGTAAGCTAATCCAAATAAAAAGC
 AGT GATGAAAGAAACACACTCATGGCAGGATTACCTACATATCCTCTGGGAGGAACCTCCAT
 CTGCTCTGGAATTAAATATGCATT CAGGTGATTGGAGAGCTACATCCCAACTCGATGGAT
 CGAAGTACTGCTGCTGACTGATGGGAGGATAACACTGCAAGTTCTGTATTGATGAAGTG
 AAACAAAGTGGGAAAGGACACGTTCTTCTCATCACATGGAACAGTCTGCCTCCAGTA
 AGAGATGAGCAAGATAACAGGAGGAAGTCATTGTTATGTTAGATGAAGCTCAGAACATG
 GCCTCATTGATGCTTTGGGGCTCTACATCAGGAAATACTGATCTCTCCCAGAACTCCCT
 CAGCTCGAAAGTAAGGGATTAAACACTGAATAGTAATGCCTGGATGAACGACACTGTCATAAT
 TGATAGTACAGTGGGAAAGGACACGTTCTTCTCATCACATGGAACAGTCTGCCTCCAGTA
 TTTCTCTGGGATCCCAGTGGAAACAATAATGGAAAATTTCACAGTGATGCAACTTCCAAA
 ATGGCCTATCTCAGTATTCCAGGAAC TGCAAAAGGTGGGACTTGGGACATACAACTTCAAGC
 CAAAGCGAACCCAGAAACATTAACTATTACAGTAACTCTCGAGCAGCAAATTCTCTGTG
 CTCCAATCACAGTGAATGCTAAAATGAATAAGGACGCTAAACAGTTCCCAAGCCAAATGATT
 GTTACGCAGAAATTCTACAAGGATATGTAACCTGTCTTGAGCCAAATGTGACTGCTTTCAT
 TGAATCACAGAATGGACATACAGAAGTTGGAACTTTGGATAATGGTGCAGCGCTGATT
 CTTCAGGAATGATGGAGTCTACTCCAGGTATTTCAGCATATACAGAAAATGGCAGATAT
 AGCTTAAAGTTGGGCTCATGGAGGAGCAAACACTGCCAGGCTAAATTACGGCCTCCACT
 GAATAGAGCCCGTACATACCAAGGCTGGTAGTGAACGGGAAATTGAAGCAAACCCGCAA
 GACCTGAAATTGATGAGGATACTCAGACCACCTGGAGGATTTCAGCGAACAGCATCCGGA
 GGTGCATTGTGGTATCACAAGTCCCAAGCCTCCCTGCCTGACCAATACCCACCAAGTC
 AATCACAGACCTGATGCCACAGTTCATGAGGATAAGATTATTCTACATGGACAGCAC
 GAGATAATTGATGTTGGAAAAGTTCAACGTTATATCATAAGAATAAGTGCAGTT
 GATCTAAGAGACAGTTGATGATGCTCTCAAGTAAATACACTGATCTGTACCAAAAGGA
 GGCAACTCCAAGGAAGCTTGCATTAAACCAGAAAATATCTCAGAAGAAAATGCAACCC
 ACATATTATTGCCATTAAAGTATAGATAAAAGCAATTGACATCAAAGTATCCAACATT
 GCACAAGTAACTTGTATCCCTCAAGCAAATCCTGATGACATTGATCCTACACCTACTCC
 TACTCCTACTCCTGATAAAAGTCATAATTCTGGAGTTAATATTCTACGCTGGTAT
 TGTCTGTGATTGGGTCTGTTGTAATTGTTACTTTATTGTTAAGTACCACTT**TGA**ACCTTA
 ACGAAGAAAAAAATCTCAAGTAGACCTAGAAGAGAGTTTAAAAACAAAATGTAAGT
 AAAGGATATTCTGAATCTAAATTACCCATGTGTGATCATAAACTCATAAAAAATT
 TTAAGATGTCGAAAAGGATACTTTGATTAAATAAAACACTCATGGATATGTAAGGACT
 CAAGATTAAATTAAATAGTTCATTTATTGTTATTGTTAAGGAAATAGTGTGAAAC
 AAAGATCCTTTCTACTGATACTGGGTGTATATTATTGATGCAACAGTTCTGAAAT
 GATATTCAAATTGCAAGAAATTAAATCATCTATCTGAGTAGTCAAAATACAAGTAA
 GGAGAGCAAATAAACACATTGGAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
 AAA

FIGURE 274

MGLFRGFVFLLVLCLLHQSN~~T~~FIKLNNNGFEDIVIVIDPSVPEDEKIIEQIEDMVTTASTY
 LFEATEK~~R~~FFFKNVSILIPENWKENPQYKRPKHENHKHADVIVAPPTLPGRDEPYTKQFTEC
 GEKGEYIHFTPD~~L~~LGKKQNEYGPPGKLFVHEWAHLRGVFDEYNEDQPFYRAKS~~K~~IEATR
 CSAGISGRNRVYKCQGGSCLSACRIDSTTKLYGKDCQFPDKVQTEKASIMFMQSIDS~~V~~VE
 FCNEKTHNQEAPSLQNIKCNFRSTWEVISNSED~~F~~KNTIPMVT~~P~~PPP~~P~~VFSLLKISQRIVCLV
 LDKSGSMGGKDRLNRMNQA~~A~~KH~~F~~LLQTVENG~~S~~WGMVHF~~D~~STATIVNKLIQIKSSDERNTLM
 AGLPTYPLGGTSICSGIKYAFQVIGELHSQ~~L~~DGEV~~L~~LDGEDNTASSCIDEVKQSGAIVH
 FIALGRAADEAVIEMSKITGGSHFYV~~S~~DEAQNNGLIDAFGALTSGNTDLSQKSLQLESKGLT
 LNSNAWMNDTVIIDSTVGKDTFFLITWNSLPPSISLWDPSGTIMENFTV~~D~~ATSKMAYLSIPG
 TAKVGTWAYNLQAKANPETLTITVTSRAANSSVPPITVN~~A~~KM~~N~~KDVNSFPSPMIVYAEILQG
 YVPVLGANVTA~~F~~IESQNGHTEVLELLDNGAGADSFKNDGV~~S~~RYFTAYTENGRYSLKVRAHG
 GANTARLKLRP~~P~~LNRAAYIPGWVN~~G~~EIEANPRPEIDEDTQTTLED~~F~~SRTASGGAFVV~~S~~QV
 PSLPLPDQYPPSQITDLDATV~~H~~E~~D~~KIILTWTAPGDNF~~D~~V~~G~~KVQRYIIRISASILDRLDSFDD
 ALQVNTTDLS~~P~~KEANSKESFAFKPENISEENATHIFIAIKSIDKSNLTSKVSNIAQVTLFIP
 QANPDDIDPTPTPTPTPDKSHNSGVNISTLVLSVIGSVVIVNFILSTTI

Signal peptide:

amino acids 1-21

Putative transmembrane domains:

amino acids 284-300, 617-633

Leucine zipper pattern.

amino acids 469-491, 476-498

N-glycosylation site.amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,
 628-632, 811-815, 832-836, 837-841, 852-856, 896-900

FIGURE 275

CTCCTTAGGTGGAAACCCCTGGGAGTAGAGTACTGACAGCAAAGACCGGGAAAGACCATACTGCCCG
 GGCAGGGGTGACAACAGGTCTATCTTTGATCTCGTGTGGCTGCCTCTATTCAAGGAAAG
 ACGCCAAGGTAATTGACCCAGAGGAGCAATGATGTAGCCACCTCTAACCTCCCTATTGAACC
 CCCAGTTATGCCAGGATTACTAGAGAGTGTCAACTCAACCAGCAAGCGGCTCCTCGGCTTAACCT
 GTGGTTGGAGGAGAGAACCTTGTGGGCTGCCTCTTAGCAGTGCTCAGAAGTGAATTGCTGA
 GGGTGGACCAGAACAGAAAGGAAAGGTCCTCTGTGCTTGGCTCACATCAGGAAGGCTGTGATGGG
 AATGAAGGTGAAAACCTGGAGATTCACTCAGTCATTGCTCTGCTGCAAGATCATCCTTAAAA
 GTAGAGAAGCTGCTCTGTGTGGTAACTCCAAGAGGCAGAACCTGTTAGAAGGAAATGGATG
 CAAGCAGCTCGGGGGCCCAAACGCATGCTTCTGTGGCTAGCCCAGGGAAAGCCCTCCGTGGG
 GCCCCGGCTTGAGGGATGCCACCGGTTCTGGACGCATGGCTGATTCCTGA**TGA**TGATGGTCC
 GGGGGCTGCTGCGTGGATTCCGGGTTGGTTTGTGGCTCTCTGCTGTGCTATCTCTGT
 CCTGTACATGTTGGCCTGCACCCAAAAGGTGACGAGGGAGCAGCTGCACTGCCCAGGGCAACAGC
 CCCACGGGAAGGAGGGGTCAAGGCCGTCCTCAGGAGTGGAGGAGCAGCACCGCAACTACGTGA
 GCAGCCTGAAGCGGAGATCGCACAGCTCAAGGAGGAGCTGCAGGAGAGGAGTGAGCAGCTCAGGAA
 TGGCAGTACCAAGCCAGCGATGCTGCTGGCTGGGCTGGACAGGAGCCCCCAGAGAACACCAG
 GCCGACCTCCTGGCCTTCGCACTCGCAGGTGGACAAGGCAGAGGTGAATGCTGGCGTCAAGCTGG
 CCACAGAGTATGCAAGCAGTGCCTTCGATAGCTTACTCTACAGAACAGGTGATACCAGCTGGAGACTGG
 CCTTACCCGCCACCCGGAGGAGAACGGCTGTGAGGAAGGACAAGCGGGATGAGTTGGTGGAGCCATT
 GAATCAGCCTGGAGGACCTGAACATCTGCAGAGAACAGCCCCAATCACCGTCTTACACGGCCT
 CTGATTTCATAGAAGGGATCTACCGAACAGAACAGGACATTGTATGAGCTCACCTCAA
 AGGGGACCAAAACACGAATTCAAACGGCTCATCTTATTGACCATTGAGCCCATATGAAAGTG
 AAAATGAAAAGCTAACATGGCAACACGCTTATCAATGTTATCGTGCCTCTAGCAAAAAGGGTGG
 ACAAGTCCGGCAGTTATGCAGAATTCAAGGAGATGTGCATTGAGCAGGATGGGAGAGTCCATCT
 CACTGTGTTACTTGGGAAAGAACAAATGAAGTCAAAGGAATACTTGAAAACACTTCCAAA
 GCTGCCAACTCAGGAATTACCTTCTGATCCAGCTGAATGGAGAATTTCCTGGGAAAGGGACTTG
 ATGTTGGAGCCGCTTCTGAAAGGAAGCAACGTCTCTCTTTCTGTGATGTGGACATCTACTT
 CACATCTGAATTCTCAATACGTGAGGCTGAATACACAGCCAGGGAAGAAGGTATTTATCCAGTT
 CTTTCAGTCAGTACAATCTGGATAATACGGCCACCATGATGCACTCCCTCCCTGGAACAGC
 AGCTGGTATAAGAAGGAAACTGGATTGGAGAGACTTGGATTGGGATGACGTGTCAGTATCG
 GTCAGACTCATCAATATAGTTGGGTTGATCTGGACATCAAAGGCTGGGGGGAGAGGATGTGCAC
 CTTTATCGCAAGTATCTCACAGAACCTCATAGTGGTACGGACCCCTGTGCGAGGACTCTCCACC
 TCTGGCATGAGAACGCGTGCATGGCAGGCTGACCCCGAGCAGTACAAGATGTGCATGCACT
 GGCCATGAACGAGGCATCCACGGCCAGCTGGCATGCTGGTGTTCAGGCACGAGATAGAGGCTCAC
 CTTCGCAAACAGAAACAGAACAGAACAGTACGAAAAAACAT**TGA**ACTCCCAGAGAAGGATTGTTGGAGA
 CACTTTTCTTCCTTTGCAATTACTGAAAGTGGCTGAAACAGAGAACAGACTTCCATAAAGGAGC
 AACAAAAGAATTGGAAGTGTGGGTCAGAGATGAGAACAGCTCGATTCTCTGTGTTGGGCTTTTAC
 AACAGAAATCAAATCTCCGTTGGCTGCAAAGTAAACCGATGTCACCCCTGTGAAGTGTCTGACA
 AAGGCAGAATGCTGTGAGGATAATAGCCTAATGGTGTGGAGGTTTGATGTTACAATACACT
 GAGACCTGTTTGTGCTCATGAAATATTGATTTAAGAGCAGTTGTAAAAAATTCA
 TAGCATGAAAGGCAAGCATATTCTCCTCATATGAATGAGCCTATCAGCAGGGCTCTAGTTCTAGG
 AATGCTAAAATATCAGAAGGCAGGAGAGGAGATAGGCTTATATGATACTAGTGAAGTACATTAA
 AAATAAAATGGACCAGAAAAGAACCAAAATGTCATATTCTCCCAAGGATTAACCA
 AAAATAATCTGCTTATCTTTGGTGTGCTTAACTGTCTCCGTTTTCTTTTAAATTTAA
 GCACTTTTCCCTGTGAGTTAGTCTGCTTATTAATTACCACTTGCACGGCTTACAAGAGA
 GCACAAAGTTGGCCTACATTATTATTTAAGAAGATACTTGGAGATGCAATTGAGACTTCA
 GTTCAAAGCATCAAATTGATGCCATATCCAAGGACATGCCAAATGCTGATTCTGTCAAGGCACTGA
 GTCAGGCATTGAGACATAGGGAAGGAATGGTTGACTAATACAGACGTACAGATACTTCTCTGAA
 GAGTATTTCGAAGAGGAGCAACTGAACACTGGAGGAAAGAACATGACACTTCTGCTTACAGAA
 AAGGAAACTCATTGAGACTGGTGTGATCTGATGTACCTAAAGTCAGAACACATTTCTCCCA
 GAAGTAGGGACCGCTTCTACCTGTTAAATAAAACCAAGTATACCGTGTGAACCAAACAATCTCT
 TTCAAAACAGGGTGTCTCCCTGGCTCTGGCTTCCATAAGAAGAAATGGGAAAGGAAATATATAT
 ATATATATATATGTGAAAGATCAATCCATCTGCCAGAATCTAGTGGGATGGAAGTTTGCTACAT
 GTTATCCACCCAGGCCAGGTGGAAGTAACTGAATTATTTAAATTAAAGCAGTTACTCAATCA
 CCAAGATGCTCTGAAAATGCATTATTACCATTCACACTTAAATTTAAATAACAGTTA
 ACATAGAGTGGTTCTCATGTAAGAACATTAGGAGCAGCACAGATGCACTGAGCTAATTATCT
 CTTTGAGTCCTGCTTGTGCTCACAGTAACCTATTGTTAAAGCTCAAGAACATTCAAGC
 TGTTGGTGTGTTAAAATGCAATTGATTGATTGACTGGTAGTTATGAAATTAAATTAAA
 AGGCCATGAATGGAAGGTGGTATTGCACAGCTAATAAAATGATTGTTGGATATGAA

FIGURE 276

MMMVRRGLLAWISRVVVLVLLCCAISVLYMLACTPKGDEEQLALPRANSPTGKEGYQAVLQEWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFLHSQVDKAEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRPEEKPVRKDKRDELVEAIESALETLNNPAENSPNRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSPIMKVNEKLNMANTLINVIVPLAKRVDKFROFMQNREMCIEQDGRVHLTVVYFGKEEINEVKGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPGKKVFYPVLFSQYNPGIIYGHDAVPPLEQQLVIKKETGFWRDFGFGMTQCYRSDFINIGGFDLDDIKGWGGEDVHLYRKYLHSNLIVVRTPVRGLFHLWHEKRCMDELTPEQYKMCMQS
KAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSSKKT

FIGURE 277

GAAAGA**ATG**TTGGCTGCTTTCTGGTACTGCCATTCATGCTGAACCTGTCAACC
 AGGTGCAGAAAATGCTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCAT
 ATGCCCTGGATACCAATGAAGAACACCTCTCAAAGCGATGGTAGCTTCTCCATGAGAAAA
 GTTCCCAACAGAGAACAGAAATTCCATGTCCTACTTGCAATGTAACCCAGAGGGT
 ATCATTCTGGTTGTGGTTACAGACCCCTCAAAAATCACACCCCTGCTGTTGAGGTGC
 AATCAGCCATAAGAACATGAACAAGAACCGGATCAACAATGCCTCTTCTAAATGACCAAAC
 CTGGAATTTAAAAATCCCTCACACTTGCAACCACCATGGACCCATCTGTGCCCATCTG
 GATTATTATATTGGTGTGATATTTGCATCATCATAGTTGCAATTGCACTACTGATTTAT
 CAGGGATCTGGCAACGTAGAACAGAACAGAACCATCTGAAGTGGATGACGCTGAAGAT
 AAGTGTGAAAACATGATCACATTGAAAATGGCATCCCTCTGATCCCTGGACATGAAGGG
 GGGCATATTAATGATGCCTTCAT**TGA**CAGAGGATGAGAGGCTCACCCCTCTGAAGGGCTGT
 TGTTCTGCTCCTCAAGAAATTAAACATTGTTCTGTGACTGCTGAGCATCCTGAAATA
 CCAAGAGCAGATCATATATTTGTTCAACCATTCTCTTGTAAATAATTGAAATGTGCT
 TGAAAGTGAAAAGCAATCAATTACCCACCAACACCACGTAAATCATAAGCTATTACGAC
 TCAAAATATTCTAAAATATTTCTGACAGTATAGTGTATAATGTGGTCATGTGGTATTG
 TAGTTATTGATTAAGCATTAGAAATAAGATCAGGCATATGTATATATTCACACTTC
 AAAGACCTAAGGAAAATAAATTCCAGTGGAGAACATATAATATGGTAGAAATCAT
 TGAAAATGGATCCTTTGACGATCACTTATATCACTCTGTATATGACTAAGTAAACAAAAG
 TGAGAAGTAATTATTGTAATGGATGGATAAAAATGGAATTACTCATATACAGGGTGGAAATT
 TTATCCTGTTATCACACCAACAGTTGATTATATTTCTGAATATCAGCCCTAATAGGAC
 AATTCTATTGTTGACCATTCTACAATTGTAAAAGTCCAATCTGTGCTAACTTAATAAG
 TAATAATCATCTTTAAAAAAAAAAAAAAAAAAAAAA

FIGURE 278

MLWLLFFLVTAIHAELCQPGAEAFKVRSLIRTALGDKAYAWDTNEEYLFKAMVAFSMRKVP
NCREATEISHVLLCNVTQRVSFWFVTDPSKNHTLPAVEVQSAIRMNKNRINNAFFLNDQTLE
FLKIPSTLAPPMDPSVPIWIIIIFGVIFCIIIVAIALLILSGIWQRRRNKEPSEVDDAEDKC
ENMITIENGIPSDPLDMKGGLMMPS

FIGURE 279

AACTCAAACCTCTCTGGAAAACGCGGTGCTTGCTCCTCCGGAGTGGCCTGGCAGG
 GTGTTGGAGCCCTCGGTCTGCCCGTCCGGTCTCTGGGCCAAGGCTGGTTCCCT**ATGT**
 ATGGCAAGAGCTCTACTCGTCGGTCTTCTCCTGGCATACAGCTCACAGCTTTGG
 CCTATAGCAGCTGTGAAATTATACTCCGGGTGCTGGAGGCTGTTAATGGGACAGATGC
 TCGGTTAAAATGCACTTCTCCAGCTTGCCCCGTGGGTGATGCTTAACAGTGACCTGGA
 ATTTTCGTCCTCTAGACGGGGACCTGAGCAGTTGTATTCTACTACCACATAGATCCCTC
 CAACCCATGAGTGGCGGTTAAGGACCGGGTGTCTGGATGGAAATCCTGAGCGGTACGA
 TGCCTCCATCCTCTGGAAACTGCAGTCGACGACAATGGGACATACACCTGCCAGGTGA
 AGAACCCACCTGATGTTGATGGGGTGTAGGGGAGATCCGGCTCAGCGTCGTGCACACTGTA
 CGCTTCTCTGAGATCCACTCCTGGCTCTGCCATTGGCTCTGCCTGTGCACTGATGATCAT
 AATAGTAATTGTAGTGGCCTCTCCAGCATTACCGAAAAAGCGATGGCCGAAAGAGCTC
 ATAAAGTGGTGGAGATAAAATCAAAGAGGAAAGGCTAACCAAGAGAAAAAGGTCTCT
 GTTTATTAGAAGACACAGAC**TAA**CAATTAGATGGAAGCTGAGATGATTCCAAGAACAA
 GAACCTAGTATTCTTGAAGTTAATGGAAACTTTCTTGGCTTTCCAGTTGTGACCGT
 TTTCCAACCAGTTCTGCAGCATATTAGATTCTAGACAAGCAACACCCCTCTGGAGCCAGCAC
 AGTGCTCCTCCATATCACCAGTCATACACAGCCTCATTATTAAGGTCTTATTAATTCA
 GTGTAATTTTCAAGTGCCTAGGTTATAAACAGAGCTACATTGGCTTAA
 GACACTACTACAGTGTATGACTTGTATACACATATATTGGTATCAAAGGGATAAAAGCC
 AATTGTCTGTTACATTCCCTCACGTATTCTTAGCAGCACTCTGCTACTAAAGTTA
 ATGTGTTACTCTTCCCTCACATTCTCAATTAAAGGTGAGCTAACGCTCCTCGGTG
 TTTCTGATTAACAGTAAATCTAAACTGTTAAATGACATTTTATTATGTCTC
 TCCTTAACATGAGACACATCTGTTACTGAATTCTCAATTCCAGGTGATAGATT
 TTTGTCG

FIGURE 280

MYGKSSTRAVLLLLGIQLTALWPIAAVEIYTSRVLEAVNGTDARLKCTFSSFAPVGDA
LTVWNFRPLDGGPEQFVFYYHIDPFQPMGRFKDRVSDGNPERYDASILLWKLQFD
DNGTYTCQVKNPPDVGVIGEIRLSVVHTVRFSEIHFLALAIGSACALMTIIVV
VVLFQHYRKRRWAERAHKVVEIKSKKEERLNQEKKVSVYLEDTD

FIGURE 281

GCATTTGTCTGTGCTCCCTGATCTTCAGGTACCCACCATGAAGTTCTTAGCAGTCCTGGT
ACTCTGGGAGTTCCATCTTCTGGTCTCTGCCAGAATCCGACAACAGCTGCTCCAGCTG
ACACGTATCCAGCTACTGGTCCTGCTGATGATGAAGCCCCCTGATGCTGAAACCAC TGCTGCT
GCAACCAC T GCG ACC ACT GCT GCT CCT ACC ACT GCA ACC ACC GCT GCT T CT ACC ACT GCT CG
TAAAGACATTCCAGTTACCAAATGGGTGGGGATCTCCGAATGGTAGAGTGTGTCCCT
GAGATGGAATCAGCTTGAGTCTTGCAATTGGTCACAACATTGCTTCCTGTGATTTC
ATCCAACTA CTTACCTTGCCTACGATATCCCCTTATCTCTAACAGTTATTTCTTCAA
ATAAAAAAATAACTATGAGCACATAAAAAAAAAAAA

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FIGURE 282

MKFLAVLVLGVSIFLVSAQNPTTAAPADTYPATGPADDEAPDAETTAATTATTAAPTTAT
TAASTTARKDIPVLPKWVGDLPNGRVCP

FIGURE 283

GGACTCTGAAGGTCCAAGCAGCTGCTGAGGCCCAAGGAAGTGGTCCAACCTGGACCC
CTAGGGGTCTGGATTGCTGGTTAACAAAGATAACCTGAGGGCAGGACCCATAGGGGA**ATGC**
TACCTCCTGCCCTTCCACCTGCCCTGGTGTACGGTGGCCTGGTCCCTGCCGAGAGA
GTGTCTGGTCAGGGACGCAGAGGACGCTCACAGACTCCAGCCTTGTTACCGAGAGGAC
ACTTGGCAAGGTCCAGCGATGGTCCGGAGTCCACACACAGACTGGCGCAGGGCAGGAGGGG
GACAGTTCTGTTGTGCTTGGTGACAGTAAGAGGGTCTTGGCCAGTCCAGGGTGGGGGCG
GCAAACCTCCATAAAGAACAGAGGGTCTGGGCCACAGAGTCATCTGCCAGCTCCT
CTGCTGCTGCCAGTGGAGTGGCACGAGGTGGGCTTGTGCCAG**TAA**AACCACAGGCTGG
ATTTGCCTGCCAGTGGCTAGGCTGTCTAGGGCAGCAATTCTAACCTTCTGCTCTCAGGA
CCCCAAAGAGCTTCATTGTATCTATTGATTTACACATTAGCAATTAAAATGAGAAAT
GGGCCGGGCACGGTGGCTCACGCCGTAAATCCCAGCACTTGGGAGGCCGAGGCCGGTGGAT
CACCTGAGATCAGGAGTTCAAGACCAGCCTGGCAACATGGTAAACCTTGTCTACTAAAAA
TACAAAAAAATTAGCCAGGCACAGTGGTGTGCACTGGTAGTCCAGTTACTCGGGAGGCTGAG
GCAGGAAAATCGCTTGAACCCAGGAGGCGGACGTTGCGGTGAGCCGAGATCGCGCCGCTGAT
TCCAGCCTGGCGACAAGAGTGAGACTCCATCTCACACA

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FIGURE 284

MLPPALPPALVFTVAWSLLAERVSVRDAEDAHLQLPFVTERTLGKVQRWSGVHTQTGGRAG
GGQFCCAWLDSKRLASPGWGAANSIKNQRVWAPATESSAQLLCCWPVGVARGGALCQ

FIGURE 285

GTC**ATG**CCAGTGCCTGCTCTGTGCCTGCTCTGGGCCCTGGCAATGGTACCCGGCCTGCCTCA
GCGGCCCCCATGGCGGCCAGAACTGGCACAGCATGAGGAGCTGACCCTGCTCTTCCATGG
GACCCTGCAGCTGGGCCAGGCCCTAACGGTGTACAGGACCACGGAGGGACGGCTGACAA
AGGCCAGGAACAGCCTGGGTCTCTATGGCCGCACAATAGAACTCCTGGGCAGGAGGTCAGC
CGGGGCCGGGATGCAGCCCAGGAACCTCGGGCAAGCCTGTTGGAGACTCAGATGGAGGAGGA
TATTCTGCAGCTGCAGGCAGAGGCCACAGCTGAGGTGCTGGGGAGGTGGCCAGGCACAGA
AGGTGCTACGGGACAGCGTGCAGCGGCTAGAAGTCCAGCTGAGGAGCGCCTGGCTGGCCCT
GCCTACCGAGAATTGAGGTCTTAAAGGCTCACGCTGACAAGCAGAGCCACATCCTATGGC
CCTCACAGGCCACGTGCAGCGCAGAGGCGGGAGATGGTGGCACAGCAGCATCGGCTGCGAC
AGATCCAGGAGAGACTCCACACAGCGCGCTCCAGCC**TGA**ATCTGCCTGGATGGAACGTGAG
GACCAATCATGCTGCAAGGAACACTTCCACGCCCGTGAGGCCCTGTGCAGGGAGGAGCTG
CCTGTTCACTGGGATCAGCCAGGGGCCGGCCCCACTTCTGAGCACAGAGCAGAGACAGAC
GCAGGGCGGGACAAAGGCAGAGGATGTAGCCCCATTGGGGAGGGTGGAGGAAGGACATGTA
CCCTTCATGCCTACACACCCCTCATTAAAGCAGAGTCGTGGCATTCAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAA

FIGURE 286

MPVPALCLLWALAMVTRPASAAPMGGPELAQHEELTLLFHGTIQLGQALNGVYRTTEGRLT
ARNSLGLYGRTIELLGQEVSRRDAAQELRASLLETQMEEDILQLQAEATAEVLGEVAQAQK
VLRDSVQRLEVQLRSAWLGPAYREFEVKAHADKOSHILWALTGHVQRQRREMAQQHRLRQ
IQERLHTAALPA

FIGURE 287

GGCAACATGGCTCAGCAGGCTTGC~~CCC~~CAGAGCCATGGCAAAGAATGGACTTGTAAATTGCAT
 CCTGGT~~G~~ATCAC~~CTT~~ACTCCTGGACCAGACCACAGCCACACATCCAGATTAAAAGCCAGGA
 AGCACAGCAAACGTCGAGTGAGAGACAAGGATGGAGATCTGAAGACTCAAATTGAAAAGCTC
 TGGACAGAAGTCAATGCCTGAAGGAAATTCAAGCCTGCAGACAGTCTGTCTCCGAGGCAC
 TAAAGTT~~C~~ACAAGAAATGCTAC~~CTT~~CAGAAGGTTGAAGCATTCCATGAGGCCAATG
 AAGACTGCATTCCAAGGAGGAATCCTGGTTATCCCCAGGA~~A~~CTCCGACGAAATCAACGCC
 CTCCAAGACTATGGTAAAAGGAGCCTGCCAGGTGTCAATGACTTTGGCTGGCATCAATGA
 CATGGTCACGGAAGGCAAGTTGTTGACGTCAACGGAATCGCTATCTCCTCCTCAACTGGG
 ACCGTGCACAGCCTAACGGTGGCAAGCGAGAAA~~A~~CTGTGTCTCTCCAA~~T~~CAGCTCAG
 GGCAAGTGGAGT~~G~~ATGAGGCCTGTCG~~C~~AGCAGCAAGAGATA~~C~~ATATGCGAGTT~~C~~ACC~~AT~~CCC
TAAATAGGTCTTCTCCAATGTGT~~C~~CTCCAAGCAAGATT~~C~~ATCATAACTTATAGGTT~~C~~ATGA
 TCTCTAAGATCAAGTAAAATCATAATT~~T~~TTACTTATTAAAAAATTGCAACACAAGATCAAT
 GTCCATAGCAATATGATAGCATCAGCCAATT~~T~~TGCTAACACACATT~~T~~TTGGATT~~T~~GCCT
 TCCTGGGTATAGGGATCAGAAATATTGATCCATGTGCACGCAGATAAA~~A~~ATGGCT~~T~~GCT
 AAACAGACTAAAAT~~T~~TTCTCTAGTCTTCACTTAGAAAAGCAAGCTTAGGCTAC~~T~~GAAAGATT
 AAATCACAGTAGCAATGCAACTCATCACTCTAGAAAAGCAAGCTTAGGCTAC~~T~~GAAAGATT
 TTCCCTGGAAGTTAGCGTATGTTGACTAACAAAAATTCCCTACATCAGAGACTCTAGGT
 GCTATATAATCCAAA~~A~~CTTT~~C~~AGCCTGTTGCTCATTCTG~~CC~~CATGCTGGCAATAATACC
 TTGTCAGCCCATTAC~~C~~CTTATT~~T~~GAATTGCTCCATCTC~~T~~GGTGGACTGTAT~~T~~TGCT
 GCCATATCAGAACACAAACCC~~T~~GAAGAGGTTCTGATTGATT~~T~~TTTTTTCTCATGCC
 TACCCTTTTGGAAAGTTCCAGCCGAATTGAAATGAAATGACAAGGTGTAT~~T~~TGAT
 CAATTTCATTCCCACCATTGCATTACAAACCTCTAACTTAAATGGTAACCCTAAGGCATAT
 CAAAGAACGAGATTGCATGATAAACGGAAATAGAAAAAAAGAACCTACATT~~T~~TTGCTT
 AGCATCCTTACTCTCAC~~TTT~~TGAGATTGAGAGTGGACTTACATT~~T~~CTTTTACATT
 TCGTATATT~~T~~TTTTAGCCATTATGTTAAGTCTATT~~T~~GGCAACCAATCT
 TGGAAGCTGAAA~~A~~CTGAATTAAAGAATGCTATCTGGAAAATTGCATACGTCTGTGCAATT
 TTTTATTCTGCCTAGTGCTATTCTGCTTAACTAGATTGTACAAAATAACTCATTGCT
 TAATATCAAATTACAAAGTTAGACTTGGAGGGAAATGGCTTTAGAAGCAAACAATT
 AAATATATT~~T~~TTGTTCTCAAATAAATAGTGTAAACATTGAATGTGTTGTGAACAAATAT
 CCCACTTGCAA~~A~~CTTA~~A~~CTACACATGCTTGGAA~~T~~TAAGTTAGCTGTT~~T~~CATTGCTCA
 ATAAT~~A~~AGCCTGAATTCTGATCAATAA~~A~~AAAAAAAAAAAAAA~~A~~AAAAAA

FIGURE 288

MAQQACPRAMAKNGLVICILVITLLLQDQTSHTSRLKARKHSKRRVRDKDGDLKTQIEKLWT
EVNALKEIQALQTVCLRGTKVHKCYLASEGLKHFHEANEDCISKGGILVIPRNSDEINALQ
DYGKRSLPGVNDFWLGINDMVTEGKFVDVNGIAISFLNWDRAQPNGGKRENCVLFQSQAQGK
WSDEACRSSKRYICEFTIPK

FIGURE 289

GCGAGGACCGGGTATAAGAAGCCTCGTGGCCTGCCCGGGCAGCCGCAGGTTCCCCGCGCGC
CCCGAGCCCCCGCGCCATGAAAGCTGCCGCCCTCCTGGGCTCTGCGTGGCCCTGTCTGCA
GCTCCGCTGCTGCTTCTTAGTGGCTCGCCAAGCCTGTGGCCAGCCTGTGCGCTGCGCTG
GAGTCGGCGGGAGGCCGGGGACCCCTGGCCAACCCCTCGGCACCCCTAACCCGCT
GAAGCTCCTGCTGAGCAGCCTGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGT
GTGTGGCTGAGCTGGTCCCCAGGCCGTGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGG
GCCCTGACAGTGTTGGCTGAGCCGAGACTGGAGCATCTACACCTGAGGACAAGACGCTGCC
CACCCGCGAGGGCTGAAAACCCCGCCGCCGGGAGGACCGTCCATCCCCTCCCCGGCCCT
CTCAATAAACGTGGTAAGAGCAAAAAAAAAAAAAAA
AAAAAAAAAAAAAA

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FIGURE 290

MKLAALLGLCVALSCSSAAFLVGSAKPVAQPVALESAAEAGAGTLANPLGTLNPLKLLS
SLGIPVNHLIEGSQKCVAELGPQAVGAVKALKALLGALTIVFG

FIGURE 291

TGAAGGACTTTCCAGGACCAAGGCCACACACTGGAAGTCTGCAGCTGAAGGGAGGCAGT
 CCTTGGCCTCCGCAGCCGATCAC**ATG**AAGGTGGTCCAAGTCTCCTGCTCTCCGTCCTCTG
 GCACAGGTGTGGCTGGTACCCGGCTTGGCCCCAGTCCTCAGTCGCCAGAGACCCCAGCCCC
 TCAGAACAGACAGCAGGGTAGTGCAGGCTCCCAGGGAGGAAGAGAAAGCCTGGCTGATGCCAGCAGGAGG
 CCAGCGAGGAGAAGGCCGGTGAGGAAGAGAAAGCCTGGCTGATGCCAGCAGGAGCAGCTT
 GCCAAGGAGACTTCAAACCTCGGATTAGCCTGCTGCGAAAGATCTCCATGAGGCACGATGG
 CAACATGGTCTTCTCCATTGGCATGTCCCTGGCATGACAGGCTGATGCTGGGGCCA
 CAGGGCCGACTGAAACCCAGATCAAGAGAGGGCTCCACTTGCAGGCCCTGAAGCCCACCAAG
 CCCGGGCTCTGCCTCCCTTTAAGGGACTCAGAGAGACCCCTCTCCGCAACCTGGAACT
 GGGCCTCTCACAGGGAGTTGCCTCATCCACAAGGATTGATGTCAAAGAGACTTCT
 TCAATTATCCAAGAGGTATTTGATACAGAGTGCCTATGAATTTCGAATGCCCTCA
 CAGGCCAAAAGGCTCATGAATCATTACATTAACAAAGAGACTCGGGGAAAATCCAAACT
 GTTTGATGAGATTAATCCTGAAACCAATTAAATTCTTGTGGATTACATCTTGTCAAAGGGA
 AATGGTTGACCCATTGACCCTGTCCTCACCGAAGTCGACACTTCCACCTGGACAAGTAC
 AAGACCATTAAAGGTGCCATGATGTACGGTGCAGGAAGTTGCCTCCACCTTGACAAGAA
 TTTTCGTTGTCATGTCCTCAAACCTGCCCTACCAAGGAATGCCACCATGCTGGTGGCCTCA
 TGGAGAAAATGGGTGACCACCTGCCCTGAAGACTACCTGACCACAGACTTGGTGGAGACA
 TGGCTCAGAAACATGAAAACCAGAAACATGGAAGTCTTCCGAAGTTCAAGCTAGATCA
 GAAGTATGAGATGCATGAGCTGCTTAGGCAGATGGGAATCAGAAGAATCTCTCACCTTG
 CTGACCTTAGTGAACTCTCAGCTACTGGAAGAAATCTCAAGTATCCAGGGTTTACGAAGA
 ACAGTGATTGAAAGTTGATGAAAGGGGACTGAGGCAGTGGCAGGAATCTTGTCAAGAAATTAC
 TGCTTATTCCATGCCCTGTCAAAAGTGGACCGGCCATTTCATTGATCTATGAAG
 AACCTCTGGAATGCTCTGTTCTGGCAGGGTGGTAATCCGACTCTCCT**TAA**TTCAAG
 ACATGCATAAGCACTCGTGTAGTAGATGCTGAATCTGAGGTATCAAACACACAGGA
 TACCAGCAATGGATGGCAGGGGAGAGTGTCCCTTGTCTAACTAGTTAGGGTGTCTC
 AAATAAAACAGTAGTCCCCACTTATCTGAGGGGATACATTCAAAGACCCCCAGCAGATGC
 CTGAAACGGTGGACAGTGTGAACCTTATATATATTCTTACACATACATACATGAT
 AAAGTTAATTATAAATTAGGCACAGTAAGAGATTAACAATAACAACATTAAGTAAA
 TGAGTTACTTGAACGCAAGCACTGCAATACCATAACAGTCAAACACTGATTATAGAGAAGGCTA
 CTAAGTGACTCATGGCGAGGAGCATAGACAGTGTGGAGACATTGGCAGGGAGAATTCA
 CATCCTGGGTGGACAGAGCAGGAGCATGCAAGATCCACTACTCAGAATGGCATGC
 TGCTTAAGACTTTAGATTGTTATTCTGGAATTTCATTAATGTTGGACCATGGT
 TGACCATGGTTAACTGAGACTGCAGAAAGCAAAACCATGGATAAGGGAGGACTACTACAAAA
 GCATTAATTGATACATTTTAAAAAAAAAAAAAA

FIGURE 292

MKVVPSSLVLLAQVWLVPGLAPSPQSPETPAPQNQTSRVVQAPREEEDEQEASEEKAGE
EEKAWLMASRQQLAKETSNGFSLLRKISMHDGNMVFSPFGMSLAMTGLMLGATGPTETQI
KRGLHLQALKPTKPGLLPSLFKGLRETLRNLELGLSQGSFAFIHKDFDVKETFFNLSKRYF
DTECVPMNFRNASQAKRLMNHYINKETRGKIPKLFDEINPETKLILVDYILFKGKWLTPFDP
VFTEVDTFHLDKYKTIVPMMYGAGKFASTFDKNFRCHVLKLPYQGNATMLVVLMEKMGDHL
ALEDYLTDLVETWLRNMKTRNMEVFFPKFKLDQYEMHELLRQMGIRRIIFSPFADLSELSA
TGRNLQVSRLRRTVIEVDERGTEAVAGILSEITAYSMPPVIKVDRPFHFMIYEETSGMLLF
LGRVVNPTLL

FIGURE 293

CTGGGATCAGCCACTGCAGCTCCCTGAGCACTCTACAGAGACGCGGACCCAGAC **ATGAG**
GAGGCTCCTCCTGGTCACCAGCCTGGTGGTTGTGCTGCTGTGGGAGGCAGGTGCAGTCCCAG
CACCCAAGGTCCCTATCAAGATGCAAGTCAAACACTGGCCCTCAGAGCAGGACCCAGAGAAG
GCCTGGGGCGCCCGTGTGGTGGAGCCTCCGGAGAAGGACGACCAGCTGGTGGTGTGCTGTTCCC
TGTCCAGAAGCCGAAACTCTTGACCACCGAGGGAGAACGCCACGAGGTCAAGGCAGGGGCCCA
TCCTTCCAGGCACCAAGGCCTGGATGGAGACCGAGGGACACCCCTGGCCGTGTCCCTGAGTCCC
GAGCCCACCATGACAGCCTGTACCACCCCTCCGCCTGAGGAGGACCAGGGCGAGGGAGGCC
CCGGTTGTGGGTGATGCCAAATCACCAGGTGCTCCTGGGACCGGAGGAAGACCAAGACCACA
TCTACCACCCCCAG **TAGGGCTCCAGGGCCATCACTGCCCGCCCTGTCCCAAGGCCAGG**
CTGTTGGGACTGGGACCCTCCCTACCCCTGCCCGAGCTAGACAAATAAACCCAGCAGGCAAA
AAAAAAAAAAAAAAA

FIGURE 294

MRRLLLVTSLVVVLLWEAGAVPAPKVKPIKMQVKHWPSEQDPEKA
WGVVEPPEKDDQLVVL
FPVQKPKLLTTEEKPRGQGRGPILPGTKAWMETEDTLGRVLSPEPDHDSLYHPP
PEEDQGEE
RPRLWVMPNHQVLLGPEEDQDHIVHPQ

FIGURE 295

AGAAAGCTGCACCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGTGAAGGAGCTCTCTG
 TACCCAAGGAAAGTCAGCTGAGACTCAGACAAGATTACA**ATG**AACCAACTCAGCTTCCCTGC
 TGTTTCTCATAGCGACCACCAAGAGGATGGAGTACAGATGAGGCTAATACTTACCAAGGAA
 TGGACCTGTTCTCGTCTCCATCTGCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCC
 TAGTGACATTGATGGCCTGTATTTCTCCGACTGAGAATGGTGTATCTACCAGACCTCT
 GTGACATGACCTCTGGGGTGGCGGCTGGACCCCTGGTGGCCAGCGTGCATGAGAATGACATG
 CGTGGGAAGTGCACGGTGGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCC
 AGAGGGGACGGCACTGGCCAACACTACAACACCTTGGATCTGCAGAGGCGGCCACGAGCG
 ATGACTACAAGAACCCCTGGCTACTACGACATCCAGGCCAAGGACCTGGCATCTGGCACGTG
 CCCAATAAGTCCCCATGCAGCACTGGAGAACAGCTCCCTGCTGAGGTACCGCACGGACAC
 TGGCTTCCTCCAGACACTGGACATAATCTGTTGGCATCTACCAGAAATATCCAGTGAAAT
 ATGGAGAAGGAAAGTGTGGACTGACAACGGCCGGTGATCCCTGTGGTCTATGATTTGGC
 GACGCCAGAAAACAGCATTACTCACCTATGGCAGCGGAATTCACTGCGGGATT
 TGTTCAGTCAGGGTATTAATAACGAGAGAGCAGCCAACGCCCTGTGTGCTGGAATGAGGG
 TCACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAGGATACTTCCAGAGGCCAGT
 CCCCAGCAGTGTGGAGATTTCTGGTTTGATTGGAGTGGATATGAACTCATGTTGGTTA
 CAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCGT**TGA**GAGTTTG
 GGAGGGAACCCAGACCTCTCCCAACCAGATGAGATCCAAGGATGGAGAACAAACTTACCC
 GTAGCTAGAATGTTAATGGCAGAAGAGAAAACAATAATCATATTGACTCAAGAAAAAAA

FIGURE 296

MNQLSFLLFLIATTRGWSTDEANTYFKEWTCSSPSLPRSCKEIKDECPSAFDGLYFLRTE
GVIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRSSQQGSKADYPEGDGNWANYNTFG
SAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSLLRYRTDTGFLQTLGHNLFGI
YQKYPVKYGECKCWTDNGPVIKVYDFGDAQKTASYSPYGQREFTAGFVQFRVFNNERAAN
ALCAGMRVTGCNTTEHHCIGGGGYFPEASPQQCGDFSGFDWSGYGTHVGYSSSREITEAAVLL
FYR

FIGURE 297

GC GG AG CC GG CG CC GG CT GC GC AG AGG AG CC G C T C G C C G C C A C C T C G G C T G G G A G C C
 C A C G A G G C T G C C G C A T C C T G C C C T C G G A A C A **ATGG** A C T C G G C G C G A G G T G C T G G G C C G
 C G C T G C T C C T G G G G A C G C T G C A G G T G C T A G C G C T G C T G G G G C C G C C A T G A A A G C G C A G C C
 A T G G C G G C A T C T G C A A A C A T A G A G A A T T C T G G G C T T C C A C A C A A C T C C A G T G C T A A C T C A A C
 A G A G A C T C T C C A A C A T G T G C C T C G A C T C C A G T A A T A C A A C G G T C A C C A C C A T G A A A C C T A C A G C G
 C A C C A A C T T C A G T T G C C T C A G T C C A G T A A T A C A A C G G T C A C C A C C A T G A A A C C T A C A G C G
 G C A T C T A A T A C A A C A A C A C C A G G G A T G G T C T C A A C A A A T A T G A C T T C T A C C A C C T T A A G T C
 T A C A C C C A A A C A A C A A C A A G T G T T C A C A G A A C A C A T C T C A G A T A T C A A C A T C C A C A A T G A C C G
 T A A C C C A C A A T A G T T C A G T G A C A T C T G C T G C T T C A T C A G T A A C A A T C A C A A C A A C T A T G C A T
 T C T G A A G C A A A G G A A A G G A T C A A A A T T G A T A C T G G G A G C T T G T T G G T A T T G T A T T A A C
 G C T G G G A G T T T A T C A T T C T T A C A T T G G A T G C A A A A T G T A T T A C T C A A G A A G A G G G C A T T C
 G G T A T C G A A C C A T A G A T G A A C A T G A T G C C A T C A T T **TAA** G G A A A T C C A T G G A C C A A G G A T G G A
 A T A C A G A T T G A T G C T G C C C T A T C A A T T A A T T T G G T T A T T A A T A G T T A A A A C A A T A T T C T
 C T T T T G A A A A T A G T A T A A A C A G G C C A T G C A T A T A A T G T A C A G T G T A T T A C G T A A A T A T G T A
 A A G A T T C T T C A A G G T A A C A A G G G T T G G G T T G A A A A T A A C A T C T G G A T C T T A T A G A C C G T
 T C A T A C A A T G G T T T A G C A A G T T C A T A G T A A G A C A A A C A A G T C C T A T C T T T T T T G G C T
 G G G G T G G G G C A T T G G T C A C A T A T G A C C A G T A A T T G A A A G A C G T C A T C A C T G A A A G A C A G A A
 T G C C A T C T G G G C A T A C A A A T A A G A A G T T G T C A C A G C A C T C A G G A T T T G G G T A T C T T T G T
 A G C T C A C A T A A A G A A C T C A G T G C T T T C A G A G C T G G A T A T A T C T T A A T T A C T A A T G C C A C A
 C A G A A A T T A T A C A A C T A A C T A G A T C T G A A G C A T A A T T A A G A A A A C A T C A A C A T T T T G
 T G C T T T A A A C T G T A G T G A T T G G T C T A G A A A C A A A A C A T C A A C A T T T T G

D E S C R I P T I O N
 1 5 6 3 4 1 5 6 3 4

FIGURE 298

MGLGARGAWAALLLGTIQLVLLGAAHESAAMAASANIENGLPHNSSANSTETLQHVPSDH
TNETSNSTVKPPTSVASDSSNTTVTTMKPTAASNTTPGMVSTNMTSTTLKSTPKTTVSQN
TSQISTSTMTVTNHNSVTSAASSVTITTMHSEAKGSKFDTGSFVGGSIVLTLGVLSILYIG
CKMYYSSRRGIRYRTIDEHDAAII

FIGURE 299

CAGCCGGGTCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCCAGCCGGAGCCGG
 TCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCGAGCGATGGCGACCCTGTGGGAGGC
 CTTCTCGGCTGGCTCCTGCTCAGCCTGTCGTGCCCTGGCGCTTCCGTGCTGCTGGC
 GCAGCTGTCAGACGCCAAGAATTGAGGATGTCAGATGTAATGTATCTGCCCTCCCT
 ATAAAGAAAATTCTGGGCATATTATAATAAGAACATATCTCAGAAAGATTGTGATTGCCTT
 CATGTTGTGGAGCCATGCCTGTGCGGGGCCTGATGTAGAACGATACTGTCTACGCTGTGA
 ATGCAAATATGAAGAAAGAACGCTCTGTACAATCAAGGTTACCATTATAATTATCTCTCCA
 TTTGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGTTGAGCCCATACTGAAGAGG
 CGCCTCTTGACATGCACAGTTGATACAGAGTGATGATATTGGGGATCACCGCCTT
 TGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAACGTGCTGAACAAGGTAG
 AATATGCACAGCAGCGCTGGAAGCTCAAGTCCAAGAGCAGCGAAAGTCTGTCTTGACCGG
 CATGTTGTCCCTCAGCTAATTGGGAATTGAATTCAAGGTGACTAGAAAGAACAGGCAGACAA
 CTGGAAAGAACTGACTGGGTTTGCTGGTTTCATTTAATACCTGTTGATTACCAACT
 GTTGCTGGAAGATTCAAAACTGGAAGCAAAACTGCTTGATTTTTCTGTTAACGTA
 ATAATAGAGACATTTAAAAGCACACAGCTCAAAGTCAGCCAATAAGTCTTCCTATTG
 TGACTTTACTAATAAAAATACTGCCTGTAAATTATCTGAAAGTCTTACCTGGAACA
 AGCACCTCTTTTACCATAGTTAACTTGACTTCAAGATAATTTCAGGGTTTG
 TTGTTGTTGTTTTGTTGTTGTTGGTGGAGAGGGAGGGATGCCTGGAAAGTGGTT
 AACAACTTTTCAAGTCACTTACTAAACAAACTTTGTAATAGACCTTACCTCTATTG
 TCGAGTTTCATTATATTGCACTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTG
 ACTTTGCACTGACTGTATTATCTGGGTATCTGCTGTCTGCACTTCATGGTAAACGGGAT
 CTAAAATGCCTGGTGGCTTTCACAAAAAGCAGATTCTTCATGTACTGTGATGTCTGATG
 CAATGCATCCTAGAACAAACTGCCATTGCTAGTTACTCTAAAGACTAAACATAGTCTG
 GTGTGTGTGGCTTACTCATTTCTAGTACCTTAAGGACAAATCTAACAGACTGGACACT
 TGCAATAAAGAAATTATTTAAACCAAGCCTCCCTGGATTGATAATATACACATTG
 TCAGCATTCCGGTCGTGGTGGAGAGGCAGCTGTTGAGCTCCAATATGTGCAAGCTTGA
 AGGGCTGGGTTGTGGTGCCTCTGAAAGGTCTAACCAATTGGATAACTGGCTTT
 TCTTCCTATGTCCTTTGAAATGTAACAATAAAATAATTGGATAACTGGCTTT

FIGURE 300

MATLWGGLRLGSLLSCLALSVLLAQLSDAAKNFEDVRCKCICPPYKENSIGHYNKNIS
QKDCDCLHVVEPMPVRGPDVAYCLRCECKYEERSSVTIKVTIIYLSILGLLLLYMVYLT
VEPILKRRLFGHAQLIQSDDDIGDHQPFANAHDLARSRSRANVLNKVEYAQQRWKLQVQE
RKSVFDRHVVLS

FIGURE 301

GCACCTGCGACCACCGTGAGCAGTCATGGCGTACTCCACAGTGCAGAGAGTCGCTCTGGCTT
CTGGGCTTGTCTGGCTCTGTCGCTGCTGCCAAGGCCTCCTGTCCCAGGGAAAGCGG
CAGGAGCCGCCGACACCTGAAGGAAAATTGGGCCGATTCCACCTATGATGCATCATCA
CCAGGCACCCTCAGATGCCAGACTCCTGGGCTCGTTCCAGAGGTCTCACCTGCCGAGG
CATTTGCAAAGGCCAAAGGATCAGGTGGAGGTGCTGGAGGAGGTAGTGGAAAGAGGTCTG
ATGGGGCAGATTATTCAATCTACGGTTGGATTTTTATATATACTGTACATTCTATT
TAAGGTAAGTAGAATCATCTAACATATTACATTGAAAATCTAATATGGCGATAAAAAA
TCATTGTCTACATTAAACTTCTTATAGTCATAAAATTATTCAAATCCATCATCTCTTTA
AATCCTGCCTCCTCTTCATGAGGTACTTAGGATAGCCATTATTCAGTTCACATAAGAATG
TTTACTCAATGTTAAGTGTGGCCAAAATTCAACAACAAGGCAGAACTAGGACTT
GAACATGGATCTTGGTCTTAATCCAGTGAGTGATACAATTCAATGCACTCCCCTGCCA

302/330

FIGURE 302

MAYSTVQRVALASGLVLALSLLLPAFLSRGKRQEPPPTPEGKLGRFPPMMHHHQAPSDGQT
PGARFQRSHLAEAFAKGSGGGAGGGSGRGLMGQIIPYFGIFLYILYILFKVSRIILI
ILHQ

FIGURE 303

CGGCTCGAGTGCAGCTGTGGGGAGATTCAGTGCATTGCCCTGGGTGCTCTCATCTT
 GGATTGAAAGTTGAGAGCAGC**ATG**TTTGCCCAGACTGAAACTCATCCTGCTGCCAGTGTAC
 TGGATTATTCCCTGGGCCTGAATGACTTGAATGTTCCCCGCTGAGCTAACAGTCCATGTG
 GGTGATTCACTCTGATGGATGTGTTCCAGAGCACAGAAGACAAATGTATATTCAAGAT
 AGACTGGACTCTGTACCAGGAGAGCACGCCAAGGACGAATATGTGCTATACTATTACTCCA
 ATCTCAGTGTGCCTATTGGCGCTTCCAGAACCGCGTACACTGATGGGGACATCTTATGC
 AATGATGGCTCTCCTGCTCCAAGATGTCAAGAGGGCTGACCAGGGAACCTATATCTGTGA
 AATCCGCCTCAAAGGGAGAGCCAGGTGTTCAAGAAGGCGGTGACTGCATGTGCTTCAG
 AGGAGCCAAAGAGCTCATGGTCATGTGGTGGATTGATTGAGATGGATGTGTTCCAG
 AGCACAGAAGTGAACACGTGACCAAGGTAGAATGGATATTCAGGACGGCGCAAAGGA
 GGAGATTGTATTCGTTACTACCACAAACTCAGGATGTCTGGAGTACTCCAGAGCTGGG
 GCCACTTCCAGAACATCGTGTGAACCTGGTGGGGACATTTCCGCAATGACGGTCCATCATG
 CTTCAAGGAGTGAGGGAGTCAGATGGAGGAAACTACACCTGCAGTATCCACCTAGGGAACCT
 GGTGTTCAAGAAAACCATTGTGCTGCATGTCAGCCCGGAAGAGCCTCGAACACTGGTACCC
 CGGCAGCCCTGAGGCCTCTGGTCTGGTGGTAATCAGTGGTGATCATTGTGGGAATTGTC
 TGTGCCACAATCCTGCTGCTCCCTGTTCTGATATTGATCGTAAGAAGACCTGTGGAAATAA
 GAGTTCAAGTGAATTCTACAGTCTGGTGAAGAACACGAAGAAGACTAATCCAGAGATAAAAG
 AAAAACCTGCCATTGAAAGATGTGAAGGGAGAAACACATTACTCCCCATAATTGTA
 CGGGAGGTGATCGAGGAAGAACCAAGTGAAAATCAGAGGCCACCTACATGACCATGCA
 CCCAGTTGGCCTCTGAGGTCAAGATCGAACACTCACTGAAAAAAAGTCAGGTGGG
 GAATGCCAAAACACAGCAAGCCTT**TGA**GAAGAATGGAGAGTCCTCATCTCAGCAGCGG
 TGGAGACTCTCCTGTGTGTCCTGGGCCACTCTACAGTGATTCACTCCCGCTCTC
 CCAGCTGTCCTCTGTCATTGTTGGTCAATACACTGAAGATGGAGAATTGGAGCCTGG
 CAGAGAGACTGGACAGCTCTGGAGGAACAGGCCTGCTGAGGGGAGGGAGCATGGACTTGGC
 CTCTGGAGTGGGACACTGGCCCTGGAACCCAGGCTGAGCTGAGTGGCCTCAAACCCCCCGTT
 GGATCAGACCCCTCTGTGGGCAGGGTTCTTAGTGGATGAGTTACTGGGAAGAACAGAGATA
 AAAACCAACCCAAATCAA

FIGURE 304

MFCPLKLILLPVLLDYSLGLNDLNVPPELTVHGDSALMGCVFQSTEDKCIFKIDWTLS
EHAKDEYVLYYYNSLSPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTYICEIRLK
GESQVFKKAVVLHVLPEEPKELMVHGGLIQMGCVFQSTEVKHVTKVEWIFSGRR
AKEEIVFRYYHKLRMSVEYSQSWGHFQNRVNLVDIFRNDGSIMLQGVRESDG
GNYTCSIHLGNLVFKKTIVLHVSPEEPRTLVTPAALRPLVLGGNQLVIIVG
IVCATILLPVLILIVKKTCGNKSSVNSTV
LVKNTKKTNPPIKEKPCHFERCEGEKHIYSPIIVREVIEEEPSEK
SEATYMTMHPVWPSLR
SDRNNNSLEKKSGGGMPKTQQAF

FIGURE 305

CTATGAAGAAGCTCCTGGAAAACAATAAGCAAAGGAAAACAAATGTGTCCCATCTCACATG
GTTCTACCCTACTAAAGACAGGAAGATCATAAACTGACAGATACTGAAATTGTAAGAGTTGG
AAACTACATTTGCAAAGTCATTGAACTCTGAGCTCAGTTGCAGTACTCGGGAAAGCC**ATGCA**
GGATGAAGATGGATACATCACCTTAAATATTAAAACCTCGGAAACCAGCTCTCGTCTCCGTTG
GCCCTGCATCCTCCTGGTGGCGTGTGATGGCTTGATTCTGCTGATCCTGTGCGTGGGG
ATGGTTGTCGGCTGGTGGCTCTGGGATTGGTCTGTCATGCAGCGCAATTACCTACAAGA
TGAGAATGAAAATCGCACAGGAACCTGCAACAATTAGCAAAGCGCTCTGTCAATATGTGG
TAAAACAATCAGAACTAAAGGGCACTTCAAAGGTCAATAATGCAGCCCCTGTGACACAAAC
TGGAGATATTATGGAGATAGCTGCTATGGGTTCTCAGGCACAACCTAACATGGGAAGAGAG
TAAGCAGTACTGCACTGACATGAATGCTACTCTCCTGAAGATTGACAACCGGAACATTGTGG
AGTACATCAAAGCCAGGACTCATTAAATTGTTGGGTCGGATTATCTGCCAGAAGTCGAAT
GAGGTCTGGAAGTGGGAGGGATGGCTCGTTATCTCAGAAAATATGTTGAGTTTTGGAAGA
TGGAAAAGGAAATATGAATTGTGCTTATTCATAATGGAAAATGCACCCCTACCTCTGTG
AGAACAAACATTATTAATGTGTGAGAGGAAGGCTGGCATGACCAAGGTGGACCAACTACCT
TAATGCAAAGAGGTGGACAGGATAACACAGATAAGGGCTTATTGTACAATAAAAGATATGT
ATGAATGCATCAGTAGCTGAAAAAAAAAAAAAA

FIGURE 306

MQDEDGYITLNIKTRKPALSVGPASSWWRVMALILLILCVGMVGLVALGIWSVMQRNYL
QDENENRTGTLQQLAKRFCQYVVKQSELKGTFKGHKCSPCDTNWRYYGDSCYFFRHNLTWE
ESKQYCTDMNATLLKIDNRNIVEYIKARTHЛИRWVGLSRQKSNEVWKWEDGSVISENMFEFL
EDGKGNMNCAYFHNGKMHPTFCENKHYLMCERKAGMTKVDQLP

FIGURE 307

CCCACGCGTCCGCGCAGTCGCGCAGTTCTGCCCTCCGCTGCCAGTCTCGCCCGCGATCCGG
 CCCGGGGCTGTGGCGTCGACTCCGACCCAGGCAGGCCAGCAGCCCAGCGCGGGAGCCGGACCGC
 CGCCGGAGGAGCTCGGACGGCATGCTGAGCCCCCTCCTTGCTGAAGCCCGAGTGCAGGAGAA
 GCCCGGGCAAACGCAGGCTAAGGAGACCAAAAGCGGCGAAGTCGCGAGACAGCGGACAAGCAG
 CGGAGGAGAAGGAGGAGGAGGCGAACCCAGAGAGGGCAGCAAAAGAAGCGGTGGTGGTGGG
 CGTCGTGGCC**ATG**GC GGCGGCTATGCCAGCTCGCTCATCCGTAGAAGAGGCAAGCCCGCG
 AGCGCGAGAAATCCAACGCCCTGCAAGTGTGTCAGCAGCCCCAGCAAAGGCAAGACCAGCTGC
 GACAAAACAAGTTAAATGTCTTCCGGTCAAACACTTCGGCTCCAAGAAGAGGCGCAG
 AAGAAGACCAGAGCCTCAGCTTAAGGGTATAGTTACCAAGCTATAAGCCGACAAGGCTACC
 ACTTGCAGCTGCAGGCGGATGGAACCATTGATGGCACCAAAGATGAGGACAGCACTTACACT
 CTGTTAACCTCATCCCTGTGGGTCTGCGAGTGGCTATCCAAGGAGTTCAAACCAAGCT
 GTACTTGGCAATGAACAGTGAGGGATACTTGTACACCTCGGAACCTTACACCTGAGTGCA
 AATTCAAAGAATCAGTGTGAAATTATTATGTGACATATTCAATGATATACCGTCAG
 CAGCAGTCAGGCCGAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATGAAAGGCAA
 CCATGTGAAGAAGAACACAAGCCTGCAGCTCATTTCTGCCTAAACCAACTGAAAGTGGCCATGT
 ACAAGGAGCCATCACTGCACGATCTCACGGAGTTCTCCGATCTGGAAGCGGGACCCAAACC
 AAGAGCAGAAGTGTCTTGGCGTGTGAACGGAGGCAAATCCATGAGCCACAATGAATCAAC
GTAGCCAGTGAGGGAAAAGAAGGGCTCTGTAACAGAACCTTACCTCCAGGTGCTGTTGAAT
 TCTTCTAGCAGTCCTCACCCAAAAGTTCAAATTGTCAGTGACATTACCAAACAAACAGG
 CAGAGTTCACTATTCTATGCCATTAGACCTTCTTATCATCCATACTAAAGC

FIGURE 308

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA28498
><subunit 1 of 1, 245 aa, 1 stop
><MW: 27564, pI: 10.18, NX(S/T): 1
MAAAIASSLIRQKRQAREREKSACKCVSSPSKGKTSCDKNKLNVFSRVKLFGSKKRRRRP
EPQLKGIVTKLYSRQGYHLQLQADGTIDGTKDEDSTYTLFNLIPVGLRVVAIQGVQTKLYLA
MNSEGYLYTSELFPECKFKESVFENYYVTYSSMIYRQQQSGRGWYLGLNKEGEIMKGNHVK
KNKPAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGPTKSRSVSGVLNGGKSMHNEST

N-glycosylation site.

amino acids 242-246

Glycosaminoglycan attachment site.

amino acids 165-169, 218-222

Tyrosine kinase phosphorylation site.

amino acids 93-100

N-myristoylation site.

amino acids 87-93, 231-237

ATP/GTP-binding site motif A (P-loop).

amino acids 231-239

HBGF/FGF family proteins

amino acids 78-94, 102-153

FIGURE 309

CCAGGATGGAGCTGGGCCTGTATGCCATTATTATTGTTCTATGCTACTAGACATGGGGGG
 ACTTGGTAAAAAGGTATTATCCAGCCAGAGGGTCTGGAGCCCTGTCTTACTGAACCTGGG
 CAACCTGGATATTCTGAGACATATTTGGGGGATTCACTGAAAAAAAGTGGGGATCCCCT
 CCATTTAGAGTGTAGCAAAGGAAAAAACACCAAGGTTGGTTCCTCCTGACATTGGCAGTG
 CCCCAGTAGGGTGGGATGAGCGAATATTCCAAAGCTAAAGTCCCACACCCTGTAGATTAC
 AAGAGTGGATTGGCAGGAGTGTGCCAAAATACAGTGGAAAGGTGCCTGAAGATATTA
 ACCACGTCTGGAAATTAGTGGGTCTGGCTTGGGATAGGTGAAGTGAGGACAGACACTG
 GAGAGGAGGGAAAGGGGACGTTCAATAGGAGGAAAATCGAGGGTGGGATCCACTGAGG
 AGTACATAGGCTGGATCTGGTGGAGCCAGCACTGGGCCACGGTGGTAAGTGGCTGCT
 GTGGAGGGGGTACGTGAGGGGGGTCTGGGCTTATCCTCAGGTCTGTGGGTGGCAG
 CGAGTCGGGCCTGAGCGTCAAGAGCATGCCCTAGTGAGCAGGCTCCTCTGGGGAGCCCAG
 CGCGCTCCGGCGCCTGCCGGTTGGGGTGTCTCCTCCGGCGCT**ATG**CGGGCGCTGGC
 CAGTAGCCTGATCCGGCAGAAGCGGGAGGTCCCGAGGCCGGGGCAGCCGGCGGTGTCGG
 CGCAGCGCGCGTGTGTCCCCCGGGCACCAAGTCCCTTGCCAGAAGCAGCTCCTCATCCTG
 CTGTCCAAGGTGCGACTGTGCCGGGGCGCCCGCGCCGGACCGCGGCCGGAGCCTCA
 GCTCAAAGGCATCGTACCAAACACTGTTCTGCCGCCAGGGTTCTACCTCCAGGGAATCCCG
 ACGGAAGCATCCAGGGCACCCAGAGGATAACCAGCTCCTCACCCACTCAACCTGATCCCT
 GTGGGCCTCCGTGGTCACCATCCAGAGCGCCAAGCTGGGTCACTACATGCCATGAATGC
 TGAGGGACTGCTACAGTTGCCGCATTCACAGCTGAGTGTGCGCTTAAGGAGTGTGTCT
 TTGAGAATTACTACGTCCGTACGCCCTGCTCTACCGCCAGCGTCGTTCTGGCCGGGCC
 TGGTACCTCGGCCTGGACAAGGAGGGCCAGGTATGAAGGGAAACCGAGTTAAGAAGACCAA
 GGCAGCTGCCACTTCTGCCAAGCTCCTGGAGGTGGCCATGTACCAGGAGCCTCTCCTCC
 ACAGTGTCCCCGAGGCCTCCCTCCAGTCCCCCTGCC**TGA**AATGTAGTCCCTGGACTG
 GAGGTTCCCTGCACTCCAGTGAGCCAGCCACCACAAACCTGT

FIGURE 310

MAALASSLIHQKREVREPGGSRPVSAQRRVCPRGTKSLCQKQLLILLSKVRLCGGRPARPDR
GPEPQLKGIVTKLFCRQGFYLQANPDGSIQGTPEDTSSFTHEFNLI PVGLRVVTIQSALKGHY
MAMNAEGLLYSSPHFTAECRFKECVFENYYVLYASALYRQRSGRAWYLGLDKEGQVMKGNR
VKKTAAAHFLPKLLEVAMYQEPLHSPVEASPSSPPAP

Tyrosine kinase phosphorylation site:

amino acids 199-207

N-myristoylation sites:

amino acids 54-60, 89-95, 131-137

HBGF/FGF family signature:

amino acids 131-155

FIGURE 311

ATGGCCGCCATCGCTAGCGGCTTGATCCGCCAGAACGGCAGGCCGGAGCAGCACTGGACCGCCGTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACCGCAGGCTCTGCAACGGCAACCTGGTGGATATCTTCTCAAAGTGCATTCGGCCTCAAGAAGCGCAGGTTGCGGCGCCAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTTGCAAATGCACCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACACTCTCAACCTCATACCAGTGGACTACGTGTTGCCATCCAGGGAGTGAAAACAGGGTTGTATAAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTACCCCTGAATGCAAGTTAAAGAATCTGTTTGAAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGGAATCTGGTAGAGCCTGGTTGGGATTAAATAAGGAAGGGCAAGCTATGAAAGGGAACAGAGTAAAGAAAACCAAACCAGCAGCTCATTTCTACCCAGCCATTGGAAGTTGCCATGTACCGAGAACCATCTTGCATGATGTTGGGAAACGGTCCCGAAGCCTGGGTGACGCCAAGTAAAAGCACAAAGTGCCTCTGCAATAATGAATGGAGGCAAACCAAGTCAACAAAGAGTAAGACAACAT**TAG**

FIGURE 312

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA28503
><subunit 1 of 1, 247 aa, 1 stop
><MW: 27702, pI: 10.36, NX(S/T): 2
MAAAIASGLIRQKRQAREQHWDRPSASRRRSSPSKNRGLCNGNLVDIFSKVRI FGLKKRRLR
RQDPQLKGIVTRLYCRQGYYLQMHPDGALDGKDDSTNSTLFNLIPVGLRVVAIQGVKTGLY
IAMNGEGLYPSELFPECKFKESVFENYYVIYSSMLYRQQESGRAWFLGLNKEQAMGNR
VKTKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASAIMNGGKPVNKSFTT
```

N-glycosylation site.

amino acids 100-104, 242-246

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 28-32, 29-33

Tyrosine kinase phosphorylation site.

amino acids 199-207

N-myristoylation site.

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

HBGF/FGF family proteins.

amino acids 104-155, 171-198

FIGURE 313

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTGGTGGTGGCTGTTGGGTGCCTTGCAAAAT
 GAAGGATGCAGGACGCAGCTTCCTGGAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGA
 ACGAACGCTTTCTGTGAGCCCTGGATCTAACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATG
 AAATAAACAGAGTTAGACCCGGGGTTGGTGTGTTCTGACATAAATAATCTAAAGCAGCTGTTCCC
 CTCCCCACCCCCAAAAAAAAGGATGATTGAAATGAAGAACCGAGGATTCAAAGAAAAAGTATGTCATT
 TTCTCTATAAAAGGAGAAAGTGAAGCCAAGGGAGATATTTGGAATGAAAAGTTGGGCTTTTAGTAAAGTAA
 AGAACTGGTGTGGGGTGTTCCTTCTTTGAATTCCCACAAGAGGAGAGGAAATTAATAACATCTGC
 AAAGAAATTTCAGAGAAGAAAAGTTGACCGCGGACATTGAGGCATTGATTGGGAGAGAACCGAGCAGAGCA
 CAGTTGGATTGTCCTATGTTGACTAAAATTGACGGATAATTGAGCTGGATTTCATCAACCTCCTT
 TTTTAAATTTATTCCCTTTGGTATCAAGATCATGCGTTCTCTGTTCTAACACCCTGGATTCCATCT
 GGATGTTGCTGTGATCAGTCTGAAATACAACACTGTTGAATTCCAGAAGGACCAACACCAGATAAATTATGA**ATG**
 TTGAACAAGATGACCTTACATCCACAGCAGATAATGATAGGTCTAGGTTAACAGGGCCATTGACCCCT
 GCTTGGTGCTGGCTGGCTCTCAACTTCTTGTGGCTGGCTGGTGCAGGGCTCAGACCTGCCCTCTGTGT
 GCTCCTGCAGCAACCAGTCAGCAAGGTGATTGTTCGGAAAACCTGCGTGAGGTTCCGGATGGCATCTCC
 ACCAACACACGGCTGCTGAACCTCCATGAGAACCAAATCCAGATCATCAAAGTGAACAGCCTCAAGCACTTGAG
 GCACCTGGAAATCCTACAGTTGAGTAGGAACCATATCAGAACCAATTGAAATTGGGCTTCATGGTCTGGCGA
 ACCTCAACACTCTGAACTCTTGACAATCGTCTTACTACCATCCCAGATGGAGCTTGTATACTGTCTAA
 CTGAAGGAGCTCTGGTGCAGAACACCCCCATTGAAAGCATCCCTCTTATGCTTTAACAGAACATTCTCTT
 GCGCCGACTAGACTAGGGAAATTGAAAAGACTTCATACATCTCAGAACGGTGCCTTGAAGGTCTGTCCA
 TGAGGTATTGAAACCTTGCCATGTGCAACCTCGGGAAATCCCTAACCTCACACCGCTCATAAA
 ACTAGATGAGCTGGATCTTCTGGAATCATTATCTGCCATCAGGCCTGGCTTTCCAGGGTTGATGCACCTCAAA
 ACTGGATGATACTGCCCAGATTCAAGTGATTGAACGGAAATGCCTTGACAAACCTTCAGTCAGTGGAGATCA
 ACCTGGCACACAATAATCTAACATTACTGCTCATGACCTCTCACTCCCTGCATCATCTAGAGCGGATACAT
 TTACATCACAACCCCTGAACTGTAACACTGTGACATACTGTGGCTCAGCTGGGATAAAAGACATGGCCCCCTC
 GAACACAGCTTGTGCCCCGTGTAACACTCCTCCAACTCTAAAGGGAGGTACATTGGAGAGCTGACCAGA
 ATTACTCACATGCTATGCTCCGGTGATTGAGGGCCCTGAGACCTCAATGTCAGTGAAGGCATGGCAGCT
 GAGCTGAAATGTCGGCCTCCACATCCCTGACATCTGTATCTGGATTACTCCAAATGAAACAGTCATGACACA
 TGGGGCGTACAAAGTGGGATAGCTGTGCTCAGTGATGGTACGTTAAATTCAAAATGAAACTGTGCAAGATA
 CAGGCATGTACACATGTATGGTGAAGTAATTCCGTTGGAAACTACTGCTCAGGCCACCTGAATGTTACTGCA
 GCAACCAACTCCTTCTTACTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGACCG
 GACCACAGATAACAATGTGGTCCCACCCAGTGGTCAGTGGAGACCACCAATGTGACCACCTCTCACAC
 CACAGAGCACAAGTCGACAGAGAAAACCTCACCCTCCAGTGGACTGATATAAACAGTGGGATCCAGGAATT
 GATGAGGTGATGAAGACTACCAAAATCATCATTGGTGTGGCATCACACTCATGGCTGCAGTGATGCT
 GGTCTTCTACAAGATGAGGAAGCAGCACCCTGGCAAAACCATCACGCCAACAGGACTGTTGAAATTA
 TTAATGTGGATGAGATTACGGGAGACACACCCATGGAAAGCCACCTGCCATGCCATGCTATCGAGCATGAG
 CACCTAAATCACTATAACTCATACAAATCTCCCTCAACCACACAACAGTTAACACAATAATTCAATACA
 CAGTTCACTGCTGAACCGTTATTGATCCGAATGAACACTCTAAAGACAATGTACAAGAGACTCAAATC**TAA**AACA
 TTTACAGAGTTACAAAAACAAACATCAAAAAAAAGACAGTTATTAAAAATGACACAAATGACTGGCTAA
 ATCTACTGTTCAAAAAAGTGTCTTACAAAAAAACAAAAAGAAAATTATTATTAATTCTATTG
 TGATCTAAAGCAGACAAAAA

FIGURE 314

MLNKMTLHPQQIMIGPRFNRALFDPLLVLLALQLVVAGLVRAQTCPSVCSCSNQFSKVIC
 VRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
 NLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPLSRRLDLGELKRLS
 YISEGAFEGLSNLRYLNLCNLREIPNLPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKL
 WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPPLHHLERIHLHHNPWCNC
 WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNTEGMAAE
 LKCRASTSLSVSWITPNGTVMTGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVSNSVGN
 TTASATLNVTAATTPFSYFSTVTETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSLTPQ
 STRSTEKTFTIPVTDINSGTIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN
 HHAPTRTVEIINVDEITGDTPMESHLPMPATEHEHLNHNSYKSPFHNTTVNTINSIHSS
 VHEPLLIRLMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.amino acids 278-282, 364-368, 390-394, 412-416, 415-419,
 434-438, 442-446, 488-492, 606-610**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
 391-397, 422-428, 433-439, 531-537

FIGURE 315

GCGCCGGGAGCCCATCTGCCCCCAGGGGCACGGGGCGCGGGGCCGCTCCGCCGGCACAT
 GGCTGCAGCCACCTCGCGCACCAGGGCGCCAGCTCGCCCGAGGTCCGTGGAG
 GGCGCCCGGCCGCCCCGGAGCCAAGCAGCAACTGAGCAGGGAAAGCGCCCGTCCGGGATC
 GGG**ATG**TCCCTCCTCCTTCCTCTGCTAGTTCTACTATGTTGGAACCTTGGGGACTCA
 CACTGAGATCAAGAGAGTGGCAGAGGAAAAGGTCACTTGCCTGCCACCATAACTGGGGC
 TTCCAGAAAAAGACACTCTGGATATTGAATGGCTGCTCACCGATAATGAAGGGAACAAAAA
 GTGGTGATCACTTACTCCAGTCGTATGTCATAAATAACTGACTGAGGAACAGAACGGCCG
 AGTGGCCTTGCCTCAATTTCCTGGCAGGAGATGCCCTTCAGATTGAACCTCTGAAGC
 CCAGTGATGAGGGCCGGTACACCTGTAAGGTTAAGAATTCAAGGCGCTACGTGTGGAGCCAT
 GTCATCTTAAAGTCTTAGTGAGACCATCCAAGCCCAGTGTGAGTTGGAAGGAGAGCTGAC
 AGAAGGAAGTGCACCTGACTTGCAGTGTGAGTCATCCTCTGGCACAGAGCCCATTGTGATT
 ACTGGCAGCGAATCCGAGAGAAAAGAGGGAGAGGATGAACGTCGCTCCCAAATCTAGGATT
 GACTACAACCACCTGGACGAGTTCTGCTGCAGAATCTTACCATGTCCTACTCTGGACTGTA
 CCAGTGCACAGCAGGCAACGAAGCTGGAAAGGAAAGCTGTGTGGTGCGAGTAACTGTACAGT
 ATGTACAAAGCATCGGCATGGTGCAGGAGCAGTGACAGGCATAGTGCTGGAGCCCTGCTG
 ATTTCTCTGGTGTGGCTGCTAATCGAAGGAAAGACAAAGAAAGATATGAGGAAGAAGA
 GAGACCTAATGAAATTGAGAAGATGCTGAAGCTCCAAAGCCGTCTGTGAAACCCAGCT
 CCTCTCCTCAGGCTCTCGGAGCTCACGCTCTGGTCTTCCACTCGCTCCACAGCAAAT
 AGTGCCTCACGCAGCCAGCAGCAGACTGTCAACTGACGCAGCACCCAGCCAGGGCTGGCAC
 CCAGGCATAACGCCTAGTGGGCCAGAGGTGAGAGGTTCTGAACCAAAGAAAGTCCACCAGT
 CTAATCTGACCAAAGCAGAAACACACCCAGCATGATCCCCAGCCAGAGCAGAGCCTTCAA
 ACGGT**TGA**ATTACAATGGACTTGACTCCACGCTTCAGGAGTCAGGGCTTGGACTC
 TTCTCGTCATTGGAGCTCAAGTCACCAGCCACACAACCAGATGAGAGGTCACTAAGTAGCA
 GTGAGCATTGACGGAACAGATTAGATGAGCATTTCCTTACAAACAAACAGCAA
 AGGATGTAAGCTGATTCTGTAAGGACATCTTATTGTGCCTTAGACCAGAGTAAGGG
 AAAGCAGGAGTCAAATCTATTGTTGACCAAGGACCTGTGGTGAGAAGGTTGGGAAAGGTG
 AGGTGAATATACTAAACTTTAATGTGGATATTGTATCAGTGCTTGATTCAA
 TTCAAGAGGAATGGATGCTGTTGTAATTTCTATGCATTCTGCAAACATTATTGGATT
 ATTAGTTATTCAAGACAGTCAAGCAGAACCCACAGCCTTATTACACCTGTCTACACCAGTAC
 TGAGCTAACCACTCTAACGAAACTCCAAAAAGGAAACATGTGCTTCTATTCTGACTTAAC
 TTCATTGTCATAAGGTTGGATATTAAATTCAAGGGAGTGAAATAGTGGAGATGGAGA
 AGAGTGAATGAGTTCTCCACTCTATACTAATCTCACTATTGTATTGAGCCAAAATAAC
 TATGAAAGGAGACAAAATTGTGACAAAGGATTGTGAAGAGCTTCCATCTCATGATGTT
 ATGAGGATTGTTGACAAACATTAGAAATATAATGGAGCAATTGTGGATTCCCCTCAAAT
 CAGATGCCTCTAAGGACTTCTGCTAGATATTCTGGAAGGAGAAACACATGTCATT
 TATCAACGTCCTTAGAAAGAATTCTTAGAGAAAAAGGGATCTAGGAATGCTGAAAGATTA
 CCCAACATACCAATTATAGTCTCTTCTGAGAAAATGTGAAACCCAGAATTGCAAGACTGG
 GTGGACTAGAAAGGGAGATTAGATCAGTTCTCTAATATGTCAAGGAAGGTAGCCGGCA
 TGGTGCCAGGCACCTGTAGGAAAATCCAGCAGGTGGAGGTTGCAGTGAGCCGAGATTATGCC
 ATTGCACTCCAGCCTGGGTGACAGAGCGGGACTCCGTCT

FIGURE 316

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419
><subunit 1 of 1, 373 aa, 1 stop
><MW: 41281, pI: 8.33, NX(S/T): 3
MSLLLLLLVSYYVGTLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV
VITYSSRHVYNLTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV
ILKVLVRPSKPCELEGELTEGSDLTLQCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID
YNHPGRVLLQNLTMYSGLYQCTAGNEAGKESCVRVTVQYVQSIGMVAGAVTGIVAGALLI
FLLVWLLIRRKDKEYEEEERPNEIREDAEAPKARLVKPSSSSGSRSSRGSSSTRSTANS
ASRSQRTLSTDAAAPQPGLATQAYSLVGPEVRGSEPKVHHANLTKAETTPSMIPSQSRAFQTV
```

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 232-251

FIGURE 317

FIGURE 318

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA82361
><subunit 1 of 1, 352 aa, 1 stop
><MW: 38938, pI: 7.86, NX(S/T): 3
MALLLCFVLLCGVVDFARSLSITTPEEMIEKAKGETAYLPCKFTLSPEDQGPLDIEWLISPA
DNQKVDQVIILYSGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVNLQLSDIGTYQCKVKK
APGVANKKIHLVVLVKPSGARCYVDGSEEIGSDFKIKCEPKEGSLPLQYEWOKLSDSQKMPT
SWLAEMTSSVISVKNASSEYSGTYSCTVRNRVGSDQCLLRLNVVPPSNKAGLIAGAIIGTLL
ALALIGLIIFCCRKKRREEKYEKEVHHDIREDVPPPKSRTSTARSYIGSNHSSLGSMSPSNM
EGYSKTQYNQVPSEDFERTPQSPTLPPAKFKYPYKTDGITVV
```

Signal sequence.

amino acids 1-19

Transmembrane domain:

amino acids 236-257

N-glycosylation sites.

amino acids 106-110, 201-205, 298-302

Tyrosine kinase phosphorylation sites.

amino acids 31-39, 78-85, 262-270

N-myristoylation sites.

amino acids 116-122, 208-214, 219-225, 237-243, 241-247,
245-251, 296-302

Myelin P0 protein.

amino acids 96-125

FIGURE 319

TGAAATGACTTCCACGGCTGGACGGGAACCTCCACCCACAGCTATGCCTCTGATTGGTGA
 ATGGTGAAGGTGCCGTCTAACCTTTCTGTAAAAAGAACCGAGCTGCCTCCAGGCAGCCAGCC
 CTCAAGCATCACTTACAGGACCAGAGGGACAAGACATGACTGTGATGAGGAGCTGCTTCGC
 CAATTTAACACCAAGAAGAATTGAGGCTGCTTGGAGGAAGGCCAGGAGGAACACGAGACTG
 AGAGATGAATTTAACAGAGGCTGCAAAGCCTGTGGACTTAGCCAGACCCTCTGCCCTC
 CTTGCTGGCGACAGCCTCTCAAATGCAGATGGTTGTGCTCCCTGCCTGGTTTACCTG
 CTTCTCTGGAGCCAGGTATCAGGGGCCAGGGCCAAGAATTCCACTTGGCCCTGCCAAGT
 GAAGGGGGTTGTTCCCCAGAAACTGTGGGAAGCCTCTGGCTGTGAAAGACACTATGCAAG
 CTCAGGATAACATCACGAGTGCCCGCTGCTGCAGCAGGAGGTTCTGCAGAACGTCTCGGAT
 GCTGAGAGCTGTTACCTGTCCACACCCCTGCTGGAGTTCTACTGAAAATGTTTCAAAAAA
 CCACACAAATAGAACAGTTGAAGTCAGGACTCTGAAGTCATTCTACTCTGCCAACAACT
 TTGTTCTCATCGTGTACAACGTCAAGAAAATGAGATGTTTCCATCAGAGAC
 AGTGCACACAGGCAGTTCTGCTATTCCGGAGAGCATTCAAACAGTGGACGTAGAACGCAGC
 TCTGACCAAAGCCCTGGGAAGTGGACATTCTGACCTGGATGCAGAAATTCTACAAGC
 TCTGAATGTCTAGACCAGGACCTCCCTCCCCCTGGCACTGGTTGTTCCCTGTGTCAATTCA
 AACAGTCTCCCTCCTATGCTGTTCACTGGACACTCAGCCCTGGCATGGTCCCATT
 TTGGCCAGGATTATTGTCAAAGAACAGTCATTCTTAAGCAGCGCCAGTGACAGTCAGGGAAAG
 GTGCCTCTGGATGCTGTGAAGAGTCTACAGAGAAGATTCTGTATTACAACTCTATT
 AATTAAATGTCAGTATTCAACTGAAGTTCTATTATTGTGAGACTGTAAGTTACATGAAGG
 CAGCAGAATATTGTCCCCATGCTCTTACCCCTACAATCCTGCCACAGTGTGGGCAG
 TGGATGGGTGCTTAGTAAGTACTTAATAAAACTGTGGTGCTTTGGCCTGTGTTGGATT
 GTTAAAAAACAGAGAGGGATGCTGGATGTAAGACTCAGAGCATGAAAATCACACT
 GTCTCTGATATCTGCAGGGACAGAGCATTGGGTGGGGTAAGGTGCATCTGTTGAAAAG
 TAAACGATAAAATGTGGATTAAAGTGCCAGCAGAACAGTCAGATCCTCAATAAACATT
 TCCCACCCACACTGCCAGCTCACCCATCATCCCTTCCCTGGTGCCTCCTTTTT
 TATCCTAGTCATTCTCCCTAAATCTCCACTTGAGTGTCAAGCTGACCTGCTGATGGTGAC
 ATTGCACCTGGATGTAATCCAATCTGTGATGACATTCCCTGCTAATAAGACAACATAA
 CTCCAAAAAAAAAAAAAAAAAAAAAA

320/330

FIGURE 320

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA88002
><subunit 1 of 1, 206 aa, 1 stop
><MW: 23799, pI: 9.12, NX(S/T): 3
MNFQQRLQSLWTLARPFCPPLLATASQMQMVLPCLGFTLLLWSQVSGAQQGQEFHFGPCQVK
GVVPQKLWEAFWAVKDTMQAQDNITSARLLQQEVLQNVSDAESCYLVHTLLEFYLKTVFKNH
HNRTVEVRTLKSFSTLANNFVLIVSQLQPSQENEMFSIRDSAHRRFLLFRRAFKQLDVEAAL
TKALGEVDILLTWMQKFYKL

Signal sequence:

amino acids 1-42

N-glycosylation sites.

amino acids 85-89, 99-103, 126-130

FIGURE 321

AAGGAGCAGCCCGAAGCACCAAGTGAGAGGCATGAAGTTACAGTGTTTCCCTTGGCTC
CTGGGTACAATACTGATATTGTGCTCAGTAGACAACCACGGTCTCAGGAGATGTCTGATTTC
CACAGACATGCACCATAAGAAGAGAGTTCCAAGAAATCAAAGAGCCATCCAAGCTAAGG
ACACCTTCCAAATGTCACTATCCTGTCCACATTGGAGACTCTGCAGATCATTAAGCCCTTA
GATGTGTGCTCGTGACCAAGAACCTCCTGGCCTACGTGGACAGGGTGTCAAGGATCA
TCAGGAGCCAACCCCCAAATCTTGAGAAAAATCAGCAGCATTGCCAActCTTCCTCTACA
TGCAGAAAActCTGCGGAATGTCAGGAACAGAGGCAGTGTCACTGCAGGCAGGAAGCCACC
AATGCCACCAGAGTCATCCATGACAActATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA
ATCCCTGGGAGAGCTCGACGTCTTAGCCTGGATTAATAAGAATCATGAAGTAATGTTCT
CAGCTTGATGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCCCTGTGCGGTTACT
GTGGGAGACAGCCCACCTTGAGGGAGGGAGATGGGAAGGGCCCTGCAGCTGAAAGTCC
CACTGGCTGGCCTCAGGCTGTCTTATTCCGCTTGAAAATAGGCAAAAGTCTACTGTGGTAT
TTGTAATAAAACTCTATCTGCTGAAAGGGCCTGCAGGCCATCCTGGAGTAAAGGGCTGCCTT
CCCATCTAATTATTGTAAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCT
GTAGTACACATTGTACTGAGTGGTTTCTGAATAAATTCCATATTTACCTATGA

FIGURE 322

```
>/usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282
><subunit 1 of 1, 177 aa, 1 stop
><MW: 20452, pI: 8.00, NX(S/T): 2
MKLQCVSLWLLGTILILCSVNDHGLRRCLISTDMHHIEESFQEIKRAIQAKDTFPNVTILST
LETLQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSFLYMQKTLRQCQEQ
RQCHCRQEATNATRVIHDNYDQLEVHAAAIKSLGELDVFLAWINKHEVMFSA
```

Signal sequence:

amino acids 1-18

N-glycosylation sites.

amino acids 56-60, 135-139

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation site.

amino acids 24-30

Actinin-type actin-binding domain signature 1.

amino acids 159-169

FIGURE 323

CCCGTGCCAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCACTGGCTCGTTAG
AACGCGGCTACAATTAATAACATAACCTTATGTATCATACACATACGATTAGGTGACACTAT
AGAATAACATCCACTTGCCTTCTCCACAGGTGTCCACTCCCAGGTCCAAC TGACACCTC
GGTTCTATCGATAATCTCAGCACCAGCCACTCAGAGCAGGGCACG **ATG**TTGGGGCCCGCCT
CAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCCTCAGAGCCTATCCA
ATGCCTCCCCACTGCTCGCTCCAGCTGGGTGGCCTGATCCACCTGTACACAGCCACAGCC
AGGAACAGCTACCACCTGCAGATCCACAAGAATGCCATGTGGATGGCGCACCCATCAGAC
CATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTGTGGTATTACAGGTGTGA
TGAGCAGAAAGATACCTCTGCATGGATTCAGAGGCAACACATTTGGATCACACTATTCGAC
CCGGAGAACTGCAGGTTCCAACACCCAGACGCTGGAAAACGGGTACGACGTCTACCACTCTCC
TCAGTATCACTCCTGGTCAGTCTGGCCGGCGAAGAGAGCCTTCCTGCCAGGCATGAACC
CACCCCCGTACTCCCAGTTCTGTCCCAGGAACGAGATCCCCCTAATTCACTAACACC
CCCATACCACGGCGGCACACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCCTGAACGT
GCTGAAGCCCCGGCCGGATGACCCCGGCCCTCCTGTTCACAGGAGCTCCGAGCG
CCGAGGACAACAGCCCAGGCCAGTGCACCCATTAGGGGTGGTCAAGGGCGGTGAGTGAAC
ACGCACGCTGGGGAACGGGCCCGAAGGCTGCCGCCCTCGCCAAGTTCATC **TAGGGTCG**
CTGG

FIGURE 324

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA142238
><subunit 1 of 1, 251 aa, 1 stop
><MW: 27954, pI: 9.22, NX(S/T): 1
MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLHYTATARNSYHLQIHKNHGVD
GAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTLENGY
DVYHSPQYHFLVSLGRAKRAFLPGMNPPPSQFLSRRNEIPLIHFNTPIP RRHTRSAEDDSE
RDPLNVLKPRARMTPAPASC SQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTGPEGCRPFA
KFI
```

Important features of the protein:

Signal peptide:

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 175-179

N-myristoylation site.

amino acids 33-39, 100-106, 225-231, 229-235

HBGF/FGF family proteins

amino acids 73-124

FIGURE 325

GGAAAAGGTACCGCGAGAGACAGCCAGCAGTCTGGAGCAGCGGTGGCCGGCTAGG**ATG**
 GGCTGTCCTGGGTCTGGCTCTGCCCTTTCTTCTGCTGGAGGTGGGTCTCTGG
 GAGCTCTGCAGGCCAGCACCGCAGAGCAGACACTGCGATGACAACGGACGACACAGAAG
 TGCCCGCTATGACTCTAGCACCGGCCACGCCCTGGAAACTCAAACGCTGAGCGCTGAG
 ACCTCTCTAGGGCCTCAACCCCAGCCGGCCCCATTCCAGAAGCAGAGACCAGGGAGCAA
 GAGAATTCCCCTGCAAGAGAGACCAGGAGTTCACAAAAACATCTCCAACTTCATGGTC
 TGATGCCACCTCCGTGGAGACATCAGCGCCAGTGGCAGCCCGAGGGAGCTGGAATGACC
 ACAGTTCAGACCATCACAGGCAGTGATCCGAGGAAGCCATTTGACACCCTTGCACCGA
 TGACAGCTCTGAAGAGGCAAAGACACTCACAATGGACATATTGACATTGGCTCACACCTCCA
 CAGAAGCTAACGGCCTGCTCAGAGAGCAGCGCCTTCCGACGGCCCCATCCAGTCATC
 ACCCGTCACGGCCTCAGAGAGCAGCGCCTTCCGACGGCCCCATCCAGTCATCACCCCC
 GTCACGGCCTCAGAGAGCAGCGCCTTCCGACGGCCCCATCCAGTCATCACCCCC
 GGTCCCCGGATCTGATGTCACTCTCCTCGCTGAAGCCCTGGTACTGTCACAAACATCGAG
 GTTATTAATTGCAGCATCACAGAAATAGAAACAACAATTCCAGCATCCCTGGGCCTCAGA
 CATAGATCTCATCCCCACGGAAGGGGTGAAGGCCTCGTCCACCTCCGATCCACAGCTCTGC
 CTGACTCCACTGAAGCAAACACACATCACTGAGGTACAGCCTCTGCCGAGACCCTGTCC
 ACAGCCGGCACCACAGAGTCAGCTGCACCTCATGCCACGGTTGGGACCCACTCCCCACTAA
 CAGGCCACAGAAAGAGAAGTGCAGCACCCGGGCCACGACCCTCAGTGGAGCTCTGGTCA
 CAGTTAGCAGGAATCCCCCTGGAAGAAACCTCAGCCCTCTGTTGAGACACCAAGTTACGTC
 AAAGTCTCAGGAGCAGCTCCGGTCTCCATAGAGGCTGGTCAGCAGTGGCAAAACAACCTC
 CTTGCTGGAGCTCTGCTCCTCCTACAGCCCTCGGAAGCCGCCCTCAAGAAACTCACCC
 CTTCAGAGACACCGACCATGGACATCGCAACCAAGGGCCCTCCCCACAGCAGGGACCC
 CTTCCCTCTGTCCTCCGACTACAACCAACAGCAGCCGAGGGACGAACAGCACCTAGCCAA
 GATCACAACCTCAGCGAAGACCAACGATGAAGCCCCAACAGCCACGCCACGACTGCCGGAC
 GAGGCCGACCACAGACG**TGA**GTGCAGGTAAAATGGAGGTTCCCTCCTGCGGCTGAGTG
 TGGCTCCCCGGAAGACCTCACTGACCCAGAGTGGCAGAAAGGCTGATGCAGCAGCTCCAC
 CGGAACTCCACGCCACGCGCCTCACTCCAGGTCTCCTACTGCGTGTCAAGGAGAGGCTA
 ACGGACATCAGCTGCAGCCAGGCATGTCCGTATGCCAAAAGAGGGTGTGCCCTAGCCTG
 GGCCCCACCGACAGACTGCAGCTCGTTACTGTGCTGAGAGGTACCCAGAAGGTTCCCATG
 AAGGGCAGCATGTCCAAGCCCTAACCCAGATGTGGCAACAGGACCCCTGCTCACATCCAC
 CGGAGTGTATGTATGGGAGGGCTTCACCTGTTCCAGAGGTGTCCCTGGACTCACCTGG
 CACATGTTCTGTGTTCAGTAAAGAGAGACCTGATCACCCATCTGTGTGCTTCCATCCTGCA
 TTAAAATTCACTCAGTGTGGCCAAAAAA

FIGURE 326

MGCLWGLALPLFFF CWEVGVSGSSAGPSTRRADTAMTTDDTEVPAMTLAPGHALETQTL SA
ETSSRASTPAGPIPEAETRGAKRISPARERSFTKTS PNFMLIATSVETSAASGSPEGAGM
TTVQTITGSDPEEAIFDTLCTDDSSEEAKTLTMDILTLAHTSTEAKGLSSESSASSDGP PHPV
ITPSRASESSASSSDGP PHPVITPSRASESSASSDG PHPVITPSWSPGS DVTLLAEALVTVTNI
EVINCSITEIE TTTSSIPGASDIDLIPTEGVKASSTS DPPALPDSTEAKPHITEVTASAETL
STAGTTESAAPHATVGTPLPTNSATEREVTAPGATTLS GALVTVSRNPLEETSALS VETPSY
VKVSGAAPVSIEAGSAVGKTTSFAGSSASSYSPSEAALKNFTPSETPTMDIATKGPFPTS RD
PLPSVPPTTNSSRGTNSTLAKITTSAKTTM KQQPRPRI.PGRGRPQT

N-glycosylation sites:

amino acids 252-256, 445-449, 451-455

cAMP-and cGMP-dependent protein kinase phosphorylation site.

amino acids 84-90

Casein kinase II phosphorylation sites.

amino acids 37-41, 108-112, 131-135, 133-137, 148-152, 165-169,
246-250, 254-258, 256-260, 269-273, 283-287, 333-337, 335-339,
404-408, 414-418, 431-435

N-myristoylation sites.

amino acids 2-8, 19-25, 117-123, 121-127, 232-238, 278-284, 314-
320, 349-355, 386-392, 397-403, 449-455

ATP/GTP-binding site motif A (P-loop).

amino acids 385-393

FIGURE 327

GCGGAGCATCCGCTCGGGCCTGCCGAGACCCCCGCGCGGATTGCCGGTCCTCCCGCG
 GCGCGACAGAGCTGCCTCGCACCTGGATGGCAGCAGGGCGCCGGGGCCTCTCGACGCCA
 GAGAGAAATCTCATCATCTGTGCAGCCTTAAAGCAAACTAAGACCAGAGGGAGGATTAT
 CCTTGACCTTGAAAGACCAAAACTAAACTGAAATTAAA**ATGTT**CTTCGGGGAGAAGGGAG
 CTTGACTTACACTTGGTAATAATTGCTTCCTGACACTAAGGCTGCTGCTAGTCAGAATT
 GCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGACATCCAGTCATCTCTTAAGGGAATC
 AGAGGCAATGAGCCGTATATACTCAACTCAAGAACACTGCATTAATTGCTGTTAAC
 AAAAAACATATCAGGGACAAAGCATGTAATTGATGATCTCGACACTCGAAAAACAGCTA
 GACAACCCAAC TGCTACCTATTTCCTGCCCCAACGAGGAAGCCTGTCATTGAAACCAGCA
 AAAGGACTTATGAGTTACAGGATAATTACAGATTTCATCTTGCACCAAGCAGTCAC
 CCAAGAGTTACCCCAGGAAGATTCTCTTACATGGCCAATTTCACAAGCAGTCAC
 TAGCCCACATCATCACACAGATTATTCAAAGCCCACCGATATCTCATGGAGAGACACACTTCT
 CAGAAGTTGGATCCTCAGATCACCTGGAGAACTATTAAAGATGGATGAAGCAAGTGC
 GCTCCTGCTTATAAGGAAAAGGCCATTCTCAGAGTTACAATTTCCTGATCAAGAAA
 TAGCTCATCTGCTGCCTGAAAATGTGAGTGCCTCCAGCTACGGTGGCAGTGCTTCT
 CATACCACCTCGGCTACTCCAAAGCCCACCCCTCTACCCACCAATGCTTCAGTGACACC
 TTCTGGGACTTCCAGCCACAGCTGGCACCCACAGCTCCACCTGTAACCACACTGTC
 AGCCTCCCACGACCCCTCATTCTACAGTTTACACGGGCTGCGGCTACACTCCAAGCAATG
 GCTACAAACAGCAGTTCTGACTACCACCTTCAGGCACCTACGGACTCGAAAGGCAGCT
 AACCATACCAGTTACAGAAATCTCAAACCTTAACTTGAACACAGGGATGTGATAACC
 CTGCACTTCTATGTCAAATGTGGAGTCTCCACTATGAATAAAACTGCTTGGGAGG
 AGGGAGGCCAGTCCAGGCAGTTCCAGGGCAGTGTCCAGAAAATCAGTACGGCCT
 ATTTGAAAATGGCTTCTTATCGGGTCCCTGCTTTGGTGTCTGGTGTAGGCC
 TCGTCCTCTGGTAGAACCTTCAGGAAATCACTCCGCAGGAAACGTTACTCAAGACTGG
 TATTGATCAATGGATCTATGTGGACATC**TAA**GGATGGAACTCGGTGTCTTAATT
 TAGTAACCAGAAGCCAAATGCAATGAGTTCTGCTGACTTGCTAGTCTAGCAGGAGGTG
 TATTGAAAGACAGGAAATGCCCTCTGCTTTCTTTTTGGAGACAGAGTCT
 GCTCTGTTGCCAGGCTGGAGTGCAGTAGCACGATCTGGCTCTACCGAACCTCC
 CTGGGTTCAAGCGATTCCCTGCCCTAGCCTCTAAGTATCTGGATTACAGGCATGTGCC
 CCACACCTGGGTATTGGTATTCTGCTTTCTTTGGAGACAGGGTTTACCATGTTGGC
 GTCTCAAACCTCTGACCTAGTGATCCACCCCTCCTGGCCTCCAAAGTGCTGGGATTACAG
 CATGAGCCACACAGCTGGCCCCCTCTGTTTATGTTGGTTTGGAGAAGGAATGAAGTG
 GGAACCAAATTAGGTAATTGGTAATCTGCTCTAAATATTAGCTAAAACAAAGCT
 ATGTAAGTAATAAAAGTATAATTGCCATATAAATTCAAACACTGGCTTTATGCAA
 GAAACAGGTTAGGACATCTAGGTCCAATTCACTTGGTCCAGATAAAATCAAC
 TGGTTATATCAATTCTAATGGATTGCTTTCTTTATGGATTCTTAAAACATTATT
 CCAGATGTAGTCCTCCAATTAAATATTGAATAATCTTGTACTCAA

FIGURE 328

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410
><subunit 1 of 1, 431 aa, 1 stop
><MW: 46810, pI: 6.45, NX(S/T): 6
MFFGGEGSLTYTLVIICFLRLSASQNCLKKSL EDVVIDIQSSLSKGIRGNEPVYTSTQED
CINS CCSTKNISGDKACNL MIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP
SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSATPKPATLL
PTNASVTPSGTSQPQLATTAPPVTTVTSQPP TTLISTVFTRAATLQAMATTAVLTTTFQAP
TDSKGSL ETIPFTEISNLT LNTGNVYNPTALSMSNVESSTMKTASWEGREASPGSSSQGSV
PENQYGLPFEKWLLIGSLLFGVLFVIGLVLLGRILSESLRRKRYSR LDYLINGIYVDI
```

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

FIGURE 329

CTCCCACGGTGTCCAGGCCAGA**ATG**CGGCTCTGGCCTGCTATGGGTTGCCTGCTGCT
 CCCAGGTTATGAAGCCCTGGAGGGCCAGAGGAATCAGCGGGTCGAAGGGGACACTGTGT
 CCCTGCAGTGCACCTACAGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGGT
 GGGATCTCTCTCGCTGCTGGCACCATCTATGCAGAAGAAGAAGGCCAGGAGACAAT
 GAAGGGCAGGGTGTCCATCCGTACAGCCGCCAGGAGCTCGCTCATTGTGACCCCTGTGGA
 ACCTCACCCCTGCAAGACGCTGGGGAGTACTGGTGTGGGTGAAACAGGGGCCGATGAG
 TCTTACTGATCTCTGTTGCTTCCAGGACCCCTGCTGCCTCCCTCCCTCCCAC
 CTTCCAGCCTCTGGCTACAACACGCCAGCAGCCAAAGCTCAGCAAACCCAGCCCC
 CAGGATTGACTTCTCTGGCTTACCCGGCAGCCACAGCCAAGCAGGGAAAGACAGGG
 GCTGAGGCCCTCCATTGCCAGGGACTTCCAGTACGGGACAGAAAGGACTTCTCAGTACAC
 AGGAACCTCTCCTCACCCAGCAGCAGCTCCTCCTGCAGGGAGCTCCGCCCTCATGCAGC
 TGGACTCCACCTCAGCAGAGGACACCAGTCCAGCTCAGCAGTGGCAGCTTAAGGCCAGG
 GTGTCCATCCCGATGGTCCGCATACTGGCCCCAGTCCAGTGGTGTGCTGAGCCTCTGTGAGC
 CGCAGGCCCTGATGCCCTCTGCAGCCACCTGCTCCTGTGGAGAAAGGAAGCTAACAGGCCA
 CGGAGACACAGAGGAACGAGAAGTTCTGGCTCTCACGCTTGACTGCGGAGGAAAAGGAAGCC
 CCTTCCCAGGCCCTGAGGGGGACGTGATCTGATGCCCTCCACACATCTGAGGAGGA
 GCTGGCTTCTGAAGTTGTCTCAGCG**TAG**GGCAGGAGGCCCTGGCCAGGCCAGCAGT
 GAAGCAGTATGGCTGGCTGGATCAGCACCGATTCCGAAAGCTTCCACCTCAGCCTCAGAG
 TCCAGCTGCCCGGACTCCAGGGCTCTCCCCACCCCTCCCAGGCTCTCCTCTTGATGTTCCA
 GCCTGACCTAGAAGCGTTGTCA GCCCTGGAGGCCAGAGCGGTGGCCTGCTCTCCGGCTG
 GAGACTGGACATCCCTGATAGGTCACATCCCTGGGAGAGTACCAAGGCTGCTGACCCTCA
 GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTCAATCTGCCAGGAACCTCTGGG
 CTCATGCCAGTGTGGACCCCTGCCCTCCACTCCAGACCCACCTTGCTCTCCCTCCC
 TGGCGTCTCAGACTTAGTCCCACGGCTCCTGCATCAGCTGGTGTGAAGAGGAGCATGCT
 GGGGTGAGACTGGATTCTGGCTCTCTTGAAACCACCTGCATCCAGCCCTTCAGGAAGCCT
 GTGAAAACGTGATTCTGGCCACCAAGACCCACCAAAACCATCTGGCTTGGTGCAG
 GACTCTGAATTCTAACATGCCAGTGACTGTCGCACTTGAGTTGAGGGCCAGTGGCCTG
 ATGAACGCTCACACCCCTCAGCTTAGAGTCTGCATTGGGCTGTGACGTCTCACCTGCC
 CAATAGATCTGCTCTGCGACACCAGATCCACGTGGGACTCCCTGAGGCCGCTGCTAAG
 TCCAGGCCTGGTCAGGTGCACATTGCAGGATAAGCCCAGGACCGGCACAGAAGTGG
 TTGCCTTNCCATTGCCCTCCCTGGNCATGCCTTCTGCCCTTGGAAAAAAATGATGAAGA
 AACCTGGCTCTTGTCTGGAAAGGGTTACTTGCTATGGTTCTGGTGGCTAGAGA
 GAAAAGTAGAAACAGAGTGCACGTAGGTGTCAACACAGAGGAGAGTAGGAACAGGGCGG
 ATACCTGAAGGTGACTCCGAGTCCAGGCCCTGGAGAAGGGCTGGGGTGGTAAAGTA
 GCACAACTACTATTTTTCTTCCATTATTATTGTTTTAAGACAGAATCTGTGCT
 GCTGCCAGGCTGGAGTGCAGTGGCACGATCTGCAAACCTCCGCTCCTGGGTCAGTGATT
 CTTCTGCCTCAGCCTCCGAGTAGCTGGGATTACAGGCACGCCACACCTGGCTAATT
 TTTGTACTTTAGTAGAGATGGGTTTACCATGTTGCCAGGCTGGCTTGAACCTCTGAC
 CTCAAATGAGCCTCTGCTTCAGTCTCCAAATTGCCGGATTACAGGCATGAGCCACTGTG
 TCTGGCCCTATTCTTTAAAAAGTGAATTAAGAGTTGTTAGTATGCAAACCTGGAAAG
 ATGGAGGAGAAAAGAAAAGGAAGAAAAAAATGTCACCCATAGTCTCACCAGAGACTATCAT
 TATTCGTTTGTGTACTTCCTCCACTTTCTTCTTCACATAATTGCCGGTGTCTT
 TTTACAGAGCAATTATCTGTATATAACATTGTATCCTGCCCTTCCACCTTAC
 ATCACTTATTCCAGCACTCTGTGTTACAGACCTTTATAAATAAAATGTTCATCA
 GCTGCATAAAAAAAAAAAA

FIGURE 330

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196
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<MW: 36143, pI: 5.89, NX(S/T): 1
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GTIYAAEEEGQETMKGRVSIRDSRQELSIVTLWNLTQDAGEYWCGVEKRGPDESLLISLFV
FPGPCCPPSPSPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGKTGAEAPPLPG
TSQYGHERTSQYTGTSPHPATSPAGSSRPPMQLDSTAEDTSPALSSGSSKPRVSIPMVRI
LAPVLVLLSLLSAAGLIAFCSHLLLWRKEAQQATETQRNEKFWLSRLTAEEKEAPSQAPEGD
VISMPPLHTSEEELGFSKFVSA
```

Important features:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128